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(54) Title: CYTOSKELETON-ASSOCIATED PROTEINS

(57) Abstract: The invention provides human cytoskeleton-associated proteins (CYSKP) and polynucleotides which identify and encode CYSKP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of CYSKP.



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CYTOSKELETON-ASSOCIATED PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of cytoskeleton-associated proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of cytoskeleton-associated proteins.

BACKGROUND OF THE INVENTION

The cytoskeleton, a cytoplasmic system of protein fibers, mediates cell shape, structure, and movement. The cytoskeleton supports the cell membrane and forms tracks along which organelles and other elements move in the cytosol. The cytoskeleton is a dynamic structure that allows cells to adopt various shapes and to carry out directed movements. Additionally, molecules can be sequestered to a specific cellular location through interaction with cytoskeleton associated proteins. Major cytoskeletal fibers are the microfilaments, the microtubules, and the intermediate filaments. Motor proteins, including myosin, dynein, and kinesin, drive movement of, or along, the fibers. Accessory or associated proteins modify the structure or activity of the fibers while cytoskeletal membrane anchors connect the fibers to the cell membrane. Other proteins associated with the cytoskeleton have roles in processes such as secretion and intracellular signaling. (The cytoskeleton is reviewed in Lodish, H. et al. (1995) Molecular Cell Biology Scientific American Books, New York NY.)

Microtubules and Associated Proteins

Tubulins

Microtubules, cytoskeletal fibers with a diameter of 24 nm, have multiple roles in the cell. Bundles of microtubules form cilia and flagella, which are whip-like extensions of the cell membrane that are necessary for sweeping materials across an epithelium and for swimming of sperm, respectively. Marginal bands of microtubules in red blood cells and platelets are important for these cells' pliability. Organelles, membrane vesicles, and proteins are transported in the cell along tracks of microtubules. For example, microtubules run through nerve cell axons, allowing bi-directional transport of materials and membrane vesicles between the cell body and the nerve terminal. Failure to supply the nerve terminal with these vesicles blocks the transmission of neural signals. Microtubules, in the form of the spindle, are also critical to chromosomal movement during cell division. Both stable and short-lived populations of microtubules exist in the cell.

Microtubules are a polymer of GTP-binding tubulin protein subunits. Each subunit is a

heterodimer of α - and β - tubulin, multiple isoforms of which exist. Alpha-tubulin undergoes a number of post-translational modifications, including acetylation, polyglutamylation, truncation of two amino acids (forming $\Delta 2$ tubulin), and tyrosination. In some cases, these modifications can affect microtubule stability. The hydrolysis of GTP is linked to the addition of tubulin subunits at the end of a
5 microtubule. The subunits interact head to tail to form protofilaments; the protofilaments interact side to side to form a microtubule. A microtubule is polarized, one end ringed with α -tubulin and the other with β -tubulin, and the two ends differ in their rates of assembly. Each microtubule is generally composed of 13 protofilaments although 11 or 15 protofilament-microtubules are sometimes found. Cilia and flagella contain doublet microtubules. Microtubules grow from specialized structures known
10 as centrosomes or microtubule-organizing centers (MTOCs). MTOCs may contain one or two centrioles, which are pinwheel arrays of triplet microtubules. The basal body, the organizing center located at the base of a cilium or flagellum, contains one centriole. γ - tubulin present in the MTOC is important for nucleating the polymerization of α - and β - tubulin heterodimers but does not polymerize into microtubules. The protein pericentrin is found in the MTOC and has a role in microtubule
15 assembly.

Microtubule-Associated Proteins

Microtubule-associated proteins (MAPs) have roles in the assembly and stabilization of microtubules. One major family of MAPs, assembly MAPs, can be identified in neurons as well as non-neuronal cells. Assembly MAPs are responsible for cross-linking microtubules in the cytosol.
20 These MAPs are organized into two domains: a basic microtubule-binding domain and an acidic projection domain. The projection domain is the binding site for membranes, intermediate filaments, or other microtubules. Based on sequence analysis, assembly MAPs can be further grouped into two types: Type I and Type II.

Type I MAPs, which include MAP1A and MAP1B, are large, filamentous molecules that co-
25 purify with microtubules and are abundantly expressed in brain and testis. They contain several repeats of a positively-charged amino acid sequence motif that binds and neutralizes negatively charged tubulin, leading to stabilization of microtubules. MAP1A and MAP1B are each derived from a single precursor polypeptide that is subsequently proteolytically processed to generate one heavy chain and one light chain.

30 Another light chain, LC3, is a 16.4 kDa molecule that binds MAP1A, MAP1B, and microtubules. It is suggested that LC3 is synthesized from a source other than the MAP1A or MAP1B transcripts, and the expression of LC3 may be important in regulating the microtubule binding activity of MAP1A and MAP1B during cell proliferation (Mann, S. S. et al. (1994) J. Biol. Chem. 269:11492-11497).

Type II MAPs, which include MAP2a, MAP2b, MAP2c, MAP4, and Tau, are characterized by three to four copies of an 18-residue sequence in the microtubule-binding domain. MAP2a, MAP2b, and MAP2c are found only in dendrites, MAP4 is found in non-neuronal cells, and Tau is found in axons and dendrites of nerve cells. Alternative splicing of the Tau mRNA leads to the existence of multiple forms of Tau protein. Tau phosphorylation is altered in neurodegenerative disorders such as Alzheimer's disease, Pick's disease, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia and Parkinsonism linked to chromosome 17. The altered Tau phosphorylation leads to a collapse of the microtubule network and the formation of intraneuronal Tau aggregates (Spillantini, M.G. and Goedert, M. (1998) Trends Neurosci. 21:428-433).

Microtubule stability may also be regulated by severing the microtubule along its length. The protein katanin, a member of the AAA adenosine triphosphatase (ATPase) superfamily, uses ATP hydrolysis energy to sever and disassemble stable microtubules. Katanin may play a role in releasing microtubules from centrosomes, regulating assembly of the mitotic spindle, and accelerating microtubule turnover during cell cycle transitions (Hartman, J.J. and Vale, R.D. (1999) Science 286:782-785).

Microtubular aggregates are associated with several disorders. An extraskeletal myxoid chondrosarcoma tumor from human contained parallel arrays of microtubules within the rough endoplasmic reticulum (Suzuki, T. et al. (1988) J. Pathol. 156:51-57). Microtubular aggregates were also found in hepatocytes from chimpanzees infected with hepatitis C virus. Monoclonal antibodies prepared to these aggregates detect a protein called p44 (or microtubular aggregates protein) (Maeda, T. et al. (1989) J. Gen. Virol. 70:1401-1407). A human homolog of p44 is inducible by interferon- α and interferon- β , but not by interferon- γ . p44 protein may be a mediator in the antiviral action of interferon (Kitamura, A. et al. (1994) Eur. J. Biochem. 224:877-883).

Dynein-related Motor Proteins

Dyneins are (-) end-directed motor proteins which act on microtubules. Two classes of dyneins exist, cytosolic and axonemal. Cytosolic dyneins are responsible for translocation of materials along cytoplasmic microtubules; for example, transport from the nerve terminal to the cell body and transport of endocytic vesicles to lysosomes. Cytoplasmic dyneins are also reported to play a role in mitosis. Axonemal dyneins are responsible for the beating of flagella and cilia. Dynein on one microtubule doublet walks along the adjacent microtubule doublet. This sliding force produces bending forces that cause the flagellum or cilium to beat. Dyneins have a native mass between 1000 and 2000 kDa and contain either two or three force-producing heads driven by the hydrolysis of ATP. The heads are linked via stalks to a basal domain which is composed of a highly variable number of accessory intermediate and light chains.

Kinesin-related Motor Proteins

Kinesins are (+) end-directed motor proteins which act on microtubules. The prototypical kinesin molecule is involved in the transport of membrane-bound vesicles and organelles. This function is particularly important for axonal transport in neurons. Kinesin is also important in all cell types for the transport of vesicles from the Golgi complex to the endoplasmic reticulum. This role is critical for maintaining the identity and functionality of these secretory organelles.

Kinesins define a ubiquitous, conserved family of over 50 proteins that can be classified into at least 8 subfamilies based on primary amino acid sequence, domain structure, velocity of movement, and cellular function. (Reviewed in Moore, J.D. and S.A. Endow (1996) *Bioessays* 18:207-219; and Hoyt, A.M. (1994) *Curr. Opin. Cell Biol.* 6:63-68.) The prototypical kinesin molecule is a heterotetramer comprised of two heavy polypeptide chains (KHCs) and two light polypeptide chains (KLCs). The KHC subunits are typically referred to as "kinesin." KHC is about 1000 amino acids in length, and KLC is about 550 amino acids in length. Two KHCs dimerize to form a rod-shaped molecule with three distinct regions of secondary structure. At one end of the molecule is a globular motor domain that functions in ATP hydrolysis and microtubule binding. Kinesin motor domains are highly conserved and share over 70% identity. Beyond the motor domain is an α -helical coiled-coil region which mediates dimerization. At the other end of the molecule is a fan-shaped tail that associates with molecular cargo. The tail is formed by the interaction of the KHC C-termini with the two KLCs.

Members of the more divergent subfamilies of kinesins are called kinesin-related proteins (KRPs), many of which function during mitosis in eukaryotes (Hoyt, *supra*). Some KRPs are required for assembly of the mitotic spindle. *In vivo* and *in vitro* analyses suggest that these KRPs exert force on microtubules that comprise the mitotic spindle, resulting in the separation of spindle poles. Phosphorylation of KRP is required for this activity. Failure to assemble the mitotic spindle results in abortive mitosis and chromosomal aneuploidy, the latter condition being characteristic of cancer cells. In addition, a unique KRP, centromere protein E, localizes to the kinetochore of human mitotic chromosomes and may play a role in their segregation to opposite spindle poles.

Microfilaments and Associated ProteinsActins

Microfilaments, cytoskeletal filaments with a diameter of 7-9 nm, are vital to cell locomotion, cell shape, cell adhesion, cell division, and muscle contraction. Assembly and disassembly of the microfilaments allow cells to change their morphology. Microfilaments are the polymerized form of actin, the most abundant intracellular protein in the eukaryotic cell. Human cells contain six isoforms of actin. The three α -actins are found in different kinds of muscle, nonmuscle β -actin and nonmuscle γ -actin are found in nonmuscle cells, and another γ -actin is found in intestinal smooth muscle cells. G-

actin, the monomeric form of actin, polymerizes into polarized, helical F-actin filaments, accompanied by the hydrolysis of ATP to ADP. Actin filaments associate to form bundles and networks, providing a framework to support the plasma membrane and determine cell shape. These bundles and networks are connected to the cell membrane. In muscle cells, thin filaments containing actin slide past thick

- 5 filaments containing the motor protein myosin during contraction. Other actin-related filaments are not part of the actin cytoskeleton, but rather associate with microtubules and dyenin.

Actin-Associated Proteins

- Actin-associated proteins have roles in cross-linking, severing, and stabilization of actin filaments and in sequestering actin monomers. Several of the actin-associated proteins have multiple
- 10 functions. Bundles and networks of actin filaments are held together by actin cross-linking proteins. These proteins have two actin-binding sites, one for each filament. Short cross-linking proteins promote bundle formation while longer, more flexible cross-linking proteins promote network formation. Calmodulin-like calcium-binding domains in actin cross-linking proteins allow calcium regulation of cross-linking. Group I cross-linking proteins have unique actin-binding domains and include the 30 Kd
- 15 protein, EF-1a, fascin, and scruin. Group II cross-linking proteins have a 7,000-MW actin-binding domain and include villin and dematin. Group III cross-linking proteins have pairs of a 26,000-MW actin-binding domain and include alpha-actinin, fimbrin, spectrin, dystrophin, ABP 120, and filamin.

- Severing proteins regulate the length of actin filaments by breaking them into short pieces or by blocking their ends. Severing proteins include gCAP39, severin (fragmin), gelsolin, and villin.
- 20 Capping proteins can cap the ends of actin filaments, but cannot break filaments. Capping proteins include CapZ, tropomodulin, and tensin.

- Tensin, which is found in focal adhesions, also crosslinks actin filaments. Integrin activation by the extracellular matrix leads to the phosphorylation of tensin on tyrosine, serine, and threonine residues; this phosphorylation also occurs in cells transformed with oncogenes. Tensin has an SH2
- 25 domain and may bind to other tyrosine-phosphorylated proteins. (Lo, S.H. et al. (1997) J. Cell Biol. 136:1349-1361.) The N-terminus of tensin contains a region homologous to the catalytic domain of a putative tyrosine phosphatase (PTP) from *Saccharomyces cerevisiae*. This PTP domain in tensin may mediate binding interactions with phosphorylated polypeptides (Haynie, D.T. and Ponting, C.P. (1996) Protein Sci. 5:2643-2646). Mice which lack the tensin gene have kidney abnormalities, indicating that
- 30 the loss of tensin leads to weakening of focal adhesions in the kidney (Lo, *supra*).

The proteins thymosin and profilin sequester actin monomers in the cytosol, allowing a pool of unpolymerized actin to exist. Profilin may also stimulate F-actin formation by effectively lowering the critical concentration required for actin monomer addition (Gertler, F.B. et al. (1996) Cell 87:227-239).

The actin-associated proteins tropomyosin, troponin, and caldesmon regulate muscle

contraction in response to calcium. The tropomyosin proteins, found in muscle and nonmuscle cells, are α -helical and form coiled-coil dimers. Striated muscle tropomyosin mediates the interactions between the troponin complex and actin, regulating muscle contraction (PROSITE PDOC00290 Tropomyosins signature). The troponin complex is composed of troponin-T, troponin-I, and troponin-C. Troponin-T binds tropomyosin, linking troponin-I and troponin-C to tropomyosin.

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Many proteins involved in the regulation of actin assembly have characteristic protein-protein interaction domains, such as for example the calponin homology (CH) domain found in actin cross-linking proteins including alpha-actinin, spectrin, and fimbrin. Other proteins which are localized primarily in focal adhesions, macromolecular complexes which mediate the contact between extracellular matrix receptors and the cytoskeleton, contain protein-protein interaction motifs known as LIM domains. For example, zyxin is a protein that plays a role in the spatial control of actin assembly and contains three tandem LIM domains. Zyxin also interacts with alpha-actinin through its proline rich N-terminus (Beckerle, M. C. (1997) BioEssays 19:949-957).

Cytoskeletal proteins are implicated in several diseases. Pathologies such as muscular dystrophy, nephrotic syndrome, and dilated cardiomyopathy have been associated with differential expression of alpha-actinin-3 (Vainzof, M. et al. (1997) Neuropediatrics 28:223-228; Smoyer, W.E. and Mundel, P. (1998) J. Mol. Med. 76:172-183; and Sussman, M.A. et al. (1998) J. Clin. Invest. 101:51-61). Alpha-actinin and several MAPs are present in Hirano bodies, which are observed more frequently in the elderly and in patients with neurodegenerative diseases such as Alzheimer's disease (Maciver, S.K. and Harrington, C.R. (1995) Neuroreport. 6:1985-1988). Actinin-4, a novel actin-bundling protein, appears to be associated with the cell motility of metastatic cancer cells. Other disease associations include premature chromosome condensation which is frequently observed in dividing cells from tumor tissue (Murnane, J.P. (1995) Cancer Metastasis Rev. 14:17-29) and the significant roles of axonemal and assembly MAPs in viral pathogenesis (Sodeik, B. et al. (1997) J. Cell Biol. 136:1007-1021).

Intermediate Filaments and Associated Proteins

Intermediate filaments (IFs) are cytoskeletal fibers with a diameter of 10 nm, intermediate between that of microfilaments and microtubules. They serve structural roles in the cell, reinforcing cells and organizing cells into tissues. IFs are particularly abundant in epidermal cells and in neurons.

IFs are extremely stable, and, in contrast to microfilaments and microtubules, do not function in cell motility. IF proteins include acidic keratins, basic keratins, desmin, glial fibrillary acidic protein, vimentin, peripherin, neurofilaments, nestin, and lamins.

IFs have a central α -helical rod region interrupted by short nonhelical linker segments. The rod region is bracketed, in most cases, by non-helical head and tail domains. The rod regions of intermediate filament proteins associate to form a coiled-coil dimer. A highly ordered assembly process leads from the dimers to the IFs. Neither ATP nor GTP is needed for IF assembly, unlike that of microfilaments and microtubules.

IF-associated proteins (IFAPs) mediate the interactions of IFs with one another and with other cell structures. IFAPs cross-link IFs into a bundle, into a network, or to the plasma membrane, and may cross-link IFs to the microfilament and microtubule cytoskeleton. Microtubules and IFs in particular are closely associated. IFAPs include BPAG1, plakoglobin, desmoplakin I, desmoplakin II, plectin, ankyrin, filaggrin, and lamin B receptor.

The N-terminal portion of ankyrin consists of a repeated 33-amino acid motif, the ankyrin repeat, which is involved in specific protein-protein interactions. Variable regions within the motif are responsible for specific protein binding, such that different ankyrin repeats are involved in binding to tubulin, anion exchange protein, voltage-gated sodium channel, Na^+/K^+ -ATPase, and neurofascin. The ankyrin motif is also found in transcription factors, such as NF- κ -B, and in the yeast cell cycle proteins CDC10, SW14, and SW16. Proteins involved in tissue differentiation, such as *Drosophila* Notch and *C. elegans* LIN-12 and GLP-1, also contain ankyrin-like repeats. Lux et al. (1990; Nature 344:36-42) suggest that ankyrin-like repeats function as 'built-in' ankyrins and form binding sites for integral membrane proteins, tubulin, and other proteins.

Cytoskeletal-Membrane Anchors

Cytoskeletal fibers are attached to the plasma membrane by specific proteins. These attachments are important for maintaining cell shape and for muscle contraction. In erythrocytes, the spectrin-actin cytoskeleton is attached to cell membrane by three proteins, band 4.1, ankyrin, and adducin. Defects in this attachment result in abnormally shaped cells which are more rapidly degraded by the spleen, leading to anemia. In platelets, the spectrin-actin cytoskeleton is also linked to the membrane by ankyrin; a second actin network is anchored to the membrane by filamin. In muscle cells the protein dystrophin links actin filaments to the plasma membrane; mutations in the dystrophin gene lead to Duchenne muscular dystrophy. In adherens junctions and adhesion plaques the peripheral membrane proteins α -actinin and vinculin attach actin filaments to the cell membrane.

IFs are also attached to membranes by cytoskeletal-membrane anchors. The nuclear lamina is attached to the inner surface of the nuclear membrane by the lamin B receptor. Vimentin IFs are

attached to the plasma membrane by ankyrin and plectin. Desmosome and hemidesmosome membrane junctions hold together epithelial cells of organs and skin. These membrane junctions allow shear forces to be distributed across the entire epithelial cell layer, thus providing strength and rigidity to the epithelium. IFs in epithelial cells are attached to the desmosome by plakoglobin and desmoplakins.

- 5 The proteins that link IFs to hemidesmosomes are not known. Desmin IFs surround the sarcomere in muscle and are linked to the plasma membrane by paranemin, synemin, and ankyrin.

Proteins of the Erythrocyte Membrane Skeleton

- Distribution of oxygen throughout the vertebrate body is effected by red blood cells (erythrocytes). Oxygen diffuses from surrounding water or from the atmosphere through either gill
10 epithelium or pulmonary epithelial type I cells. Oxygen then diffuses through the blood capillary endothelium directly to the blood circulatory system and through the erythrocyte membrane and is stored as soluble oxyhemoglobin in the cytoplasm. Oxygen is released from hemoglobin at sites throughout the organism and diffuses out from the erythrocyte to other target cells. The structure of the erythrocyte membrane as well as that of other non-erythrocyte cells must be maintained to enable
15 efficient diffusion of oxygen to intracellular compartments.

- The erythrocyte membrane is comprised of i) a cholesterol-rich phospholipid bilayer in which many trans-bilayer proteins are embedded, ii) external glycosylphosphatidylinositol-anchored proteins (GPI-proteins), and iii) the erythrocyte or membrane skeleton that laminates the inner surface of the bilayer. The trans-bilayer proteins include anion exchangers, glycophorins, glucose transporters, and a
20 variety of cation transporters and pumps. The erythrocyte GPI-proteins include acetylcholinesterase and decay-accelerating factor (CD 55). The skeletal proteins are organized on the cortical, or cytoplasmic, face of the plasma membrane. These proteins include protein 4.1, protein p55, α - and β -spectrin, actin, and actin-binding proteins such as dematin, tropomyosin, and tropomodulin. α - and β -spectrin combine to form a heterotetramer in vivo. The spectrin heterotetramer organizes into a cortical
25 bidimensional network with a hexagonal mesh. The network is linked to trans-bilayer proteins through a protein complex comprising β -spectrin, ankyrin, anion exchanger, and protein 4.2 and through the "triangular" interaction between protein 4.1, glycophorin C, and protein p55. Structural and functional variants of erythrocyte membrane proteins have been found in a variety of tissues. Variants may be transcribed from multigene families, e.g., anion exchanger, ankyrin, or spectrin, or from single
30 gene families, e.g., protein 4.1 or protein 4.2. mRNA transcripts undergo tissue-specific alternative splicing. Many congenital hemolytic anemias result from mutations in the above-mentioned genes encoding erythrocyte membrane proteins. For example, hereditary elliptocytosis stems from an array of mutations in the spectrin genes at or near the head-to-head self-association region of the spectrin tetramer, or from mutations in the protein 4.1 gene which reduce levels of protein 4.1. In another

example, hereditary spherocytosis is associated with mutations in the ankyrin gene, the anion exchanger gene, the protein 4.2 gene, or the α - and β -spectrin genes. (Delaunay J. (1995) Transfus. Clin. Biol. 2:207-216.)

Protein 4.1 is an 80 kDa erythrocyte membrane protein with four functional domains. These domains include: i) a 30 kDa basic N-terminal domain, homologous to the ERM (Ezrin/Radixin/Moesin) family of actin- and transmembrane protein-binding proteins (Tsukita, S. et al. (1997) Trends Biochem. Sci. 22:53-58); ii) a 16 kDa hydrophilic domain containing a protein kinase C phosphorylation site; iii) a 10 kDa highly charged domain containing a cAMP-dependent protein kinase phosphorylation site critical for the interaction with spectrin and actin; and iv) a 22/24 kDa acidic domain. Protein 4.1 is a member of a structurally and functionally related protein 4.1 family. The protein 4.1 family is part of an evolutionarily related protein superfamily that includes many tyrosine phosphatases. (Baklouti, F. et al. (1997) Genomics 39:289-302.)

In contrast to the strictly cortical localization of protein 4.1 in mature enucleate erythrocytes, protein 4.1 epitopes have been observed throughout the cytoplasmic compartment and the nucleoskeleton in nucleated cells. In particular, protein 4.1 is present in the nucleoskeleton during interphase, in the mitotic spindle during mitosis, in perichromatin during telophase, and in the midbody during cytokinesis. (Krauss, S.W. et al. (1997) J. Cell Biol. 137:275-289.)

Differential expression of the protein 4.1 gene resulting in a number of mRNA splice variants has been observed in various human and rodent tissues. Comparison of the gene structure and mRNA splice variants revealed the extreme genomic sequence conservation of protein 4.1 between different species. The 5' UTR of both the human and rodent mRNA species has not been successfully identified and sequenced, possibly due to GC-rich regions therein which give rise to technical complications during nucleotide sequencing reactions. (Baklouti, supra; Conboy, J.G. (1988) Proc. Natl. Acad. Sci. 85:9062-9065.)

Analysis of proteins included in the ERM family of proteins has indicated that the N-terminal domain interacts with intracellular domains of transmembrane proteins such as CD44 and the C-terminal domain binds actin. Both interactions involve interactions with Rho-GTP protein complex, polyphosphoinositides, and serine/threonine kinase and tyrosine kinase activities. Many of the phosphorylation sites on ERM proteins are conserved. Although expression of ERM proteins *in vivo* is restricted to tissues such as endothelium, repression of ERM protein gene expression is released under conditions of cell culture. (Tsukita, supra.)

The cortical actin cytoskeleton participates in various membrane-based processes which necessitate a large amount of functional plasticity in the molecular components involved. A family of proteins homologous to band 4.1 is involved in the reorganization of the actin cytoskeleton in response

to various stimuli and probably plays a role in transmembrane signaling. This family includes tyrosine phosphatases, substrates of tyrosine kinases and a candidate for a tumor-suppressor gene. (Arpin M, et al. (1994) Curr. Opin. Cell Biol. 6:136-141.)

Disruptions in cytoskeletal protein interaction have been identified in a number of disease
 5 conditions or disorders. Neurofibromatosis type 2 is an autosomal dominant disease of the nervous system. Schwann cells isolated from patients with neurofibromatosis type 2 have characteristic morphology and growth parameters which differ from control Schwann cells. A gene associated with neurofibromatosis type 2 has been identified and is termed NF2. The NF2 gene product, known as schwannomin or merlin, is a member of the protein 4.1 superfamily, and mutations in the NF2 gene
 10 have been shown to be associated with the disease. (Rosenbaum, C. et al. (1998) Neurobiol. Dis. 5:55-64.) In addition, a form of psoriasis may be due to altered expression or distribution in epidermal epithelium of analogs of erythrocyte protein 4.1. (Shimizu, T. (1996) Histol. Histopathol. 11:495-501.) Erythrocytes carrying mutations in spectrin and protein 4.1 showed differing sensitivities to invasion by Plasmodium falciparum. (Facer, C.A. (1995) Parasitol Res. 81:52-57.) Furthermore, antibodies raised
 15 against erythrocyte protein 4.1 stained the majority of neurofibrillary tangles in the prefrontal cortex and hippocampus of brain tissue from patients with Alzheimer's disease. A 68 kDa protein was identified as the most likely brain analog of erythrocyte protein 4.1. (Sihag, R.K. et al. (1994) Brain Res. 656:14-26.)

The discovery of new cytoskeleton-associated proteins and the polynucleotides encoding them
 20 satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of cytoskeleton-associated proteins.

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SUMMARY OF THE INVENTION

The invention features purified polypeptides, cytoskeleton-associated proteins, referred to collectively as "CYSKP" and individually as "CYSKP-1," "CYSKP-2," "CYSKP-3," "CYSKP-4," "CYSKP-5," "CYSKP-6," "CYSKP-7," "CYSKP-8," "CYSKP-9," "CYSKP-10," "CYSKP-11,"
 30 "CYSKP-12," "CYSKP-13," "CYSKP-14," "CYSKP-15," "CYSKP-16," "CYSKP-17," "CYSKP-18," "CYSKP-19," "CYSKP-20," "CYSKP-21," "CYSKP-22," "CYSKP-23," "CYSKP-24," "CYSKP-25," "CYSKP-26," "CYSKP-27," "CYSKP-28," "CYSKP-29," "CYSKP-30," "CYSKP-31," "CYSKP-32," "CYSKP-33," and "CYSKP-34." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence

selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic
5 fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-34.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group
10 consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. In one
15 alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-34. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:35-68.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting
20 of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino
25 acid sequence selected from the group consisting of SEQ ID NO:1-34. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of
30 SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The method comprises a)

culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a

5 polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic

10 fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90%

15 identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample,

20 said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the

25 sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of

30 said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID

NO:35-68, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional CYSKP, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional CYSKP, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring

polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional CYSKP, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in

altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:35-68, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

- 5 The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, ii) a
- 10 naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in
- 15 the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, ii) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the
- 20 polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated
- 25 biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

- 30 Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

- Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of
- 35 the polypeptides.

Table 4 lists the cDNA and genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

5 Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

10 DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will
15 be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so
20 forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described.
25 All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

30 "CYSKP" refers to the amino acid sequences of substantially purified CYSKP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of CYSKP. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other

compound or composition which modulates the activity of CYSKP either by directly interacting with CYSKP or by acting on components of the biological pathway in which CYSKP participates.

An "allelic variant" is an alternative form of the gene encoding CYSKP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

- 10 "Altered" nucleic acid sequences encoding CYSKP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as CYSKP or a polypeptide with at least one functional characteristic of CYSKP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding CYSKP, and improper or unexpected hybridization to allelic variants, with
15 a locus other than the normal chromosomal locus for the polynucleotide sequence encoding CYSKP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent CYSKP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the
20 biological or immunological activity of CYSKP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and
25 valine; glycine and alanine; and phenylalanine and tyrosine.

- The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence
30 to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of

CYSKP. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of CYSKP either by directly interacting with CYSKP or by acting on components of the biological pathway in which CYSKP participates.

- 5 The term “antibody” refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind CYSKP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or
10 synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

- The term “antigenic determinant” refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to
15 immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

- The term “antisense” refers to any composition capable of base-pairing with the “sense”
20 (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense
25 molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation “negative” or “minus” can refer to the antisense strand, and the designation “positive” or “plus” can refer to the sense strand of a reference DNA molecule.

- 30 The term “biologically active” refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, “immunologically active” or “immunogenic” refers to the capability of the natural, recombinant, or synthetic CYSKP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

“Complementary” describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A “composition comprising a given polynucleotide sequence” and a “composition comprising a given amino acid sequence” refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding CYSKP or fragments of CYSKP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus sequence” refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

“Conservative amino acid substitutions” are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
25	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
30	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
35	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr

Thr	Ser, Val
Trp	Phe, Tyr
Tyr	His, Phe, Trp
Val	Ile, Leu, Thr

5

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

10

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

15

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

20

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

A "fragment" is a unique portion of CYSKP or the polynucleotide encoding CYSKP which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

35

A fragment of SEQ ID NO:35-68 comprises a region of unique polynucleotide sequence that

specifically identifies SEQ ID NO:35-68, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:35-68 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:35-68 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:35-68 and the region of SEQ ID NO:35-68 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-34 is encoded by a fragment of SEQ ID NO:35-68. A fragment of SEQ ID NO:1-34 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-34. For example, a fragment of SEQ ID NO:1-34 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-34. The precise length of a fragment of SEQ ID NO:1-34 and the region of SEQ ID NO:1-34 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search

Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions,

explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment
5 program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

10 Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

15 *Gap x drop-off: 50*

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for
20 example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to
25 describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid
30 sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity.

Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of CYSKP which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of CYSKP which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of CYSKP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of CYSKP.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an CYSKP may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by

cell type depending on the enzymatic milieu of CYSKP.

"Probe" refers to nucleic acid sequences encoding CYSKP, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical
5 labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

10 Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the
15 specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR
20 Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such
25 purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South
30 West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for

microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that
5 hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary
10 polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the
15 artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

20 Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs).
25 Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and
30 other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing CYSKP, nucleic acids encoding CYSKP, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

5 The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope
10 A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

 The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which
15 they are naturally associated.

 A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers,
20 microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

 A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

 "Transformation" describes a process by which exogenous DNA is introduced into a recipient
25 cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells"
30 includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

 A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic

acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in
5 vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention
10 into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999)
15 set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant
20 identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic
25 variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at
30 least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a

certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human cytoskeleton-associated proteins (CYSKP), the polynucleotides encoding CYSKP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are cytoskeleton-associated proteins. For example, SEQ ID NO:31 is 34% identical to a *Caenorhabditis elegans* protein similar to mouse ankyrin

(GenBank ID g3879121) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 1.1×10^{-146} , which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:31 also contains Ank repeats as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. As a second example, SEQ ID NO:34 is 96% identical over 97 amino acids to human Intermediate Filament Associated Protein (GenBank ID 1333846) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 8.2×10^{-45} , which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. Data from BLAST analyses using the PRODOM database provide further corroborative evidence that SEQ ID NO:34 is a cytoskeleton protein. (See Table 3.) SEQ ID NO:1-30 and SEQ ID NO:32-33 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-34 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:35-68 or that distinguish between SEQ ID NO:35-68 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 3824958H1 is the identification number of an Incyte cDNA sequence, and BRAXNOT01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71263527V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g2276318) which contributed to the assembly of the full length polynucleotide sequences. Alternatively, the identification numbers in column 5 may refer to coding regions predicted by Genscan analysis of genomic DNA. The Genscan-predicted coding sequences may

have been edited prior to assembly. (See Example IV.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. (See Example V.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon-stretching" algorithm. (See Example V.) In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses CYSKP variants. A preferred CYSKP variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the CYSKP amino acid sequence, and which contains at least one functional or structural characteristic of CYSKP.

The invention also encompasses polynucleotides which encode CYSKP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:35-68, which encodes CYSKP. The polynucleotide sequences of SEQ ID NO:35-68, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding CYSKP. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding CYSKP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:35-68 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:35-68. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of CYSKP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding CYSKP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the

invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring CYSKP, and all such variations are to be considered as being specifically disclosed.

5 Although nucleotide sequences which encode CYSKP and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring CYSKP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding CYSKP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide
10 occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CYSKP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

15 The invention also encompasses production of DNA sequences which encode CYSKP and CYSKP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding CYSKP or any fragment thereof.

20 Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:35-68 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in
25 "Definitions."

 Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or
30 combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing

system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

- The nucleic acid sequences encoding CYSKP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060).
- Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

- When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-

specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer
5 controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode CYSKP may be cloned in recombinant DNA molecules that direct expression of CYSKP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of
10 the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express CYSKP.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter CYSKP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA
15 shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such
20 as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of CYSKP, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene
25 variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random
30 point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding CYSKP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser.* 7:215-223; and Horn, T. et al. (1980) *Nucleic Acids Symp. Ser.* 7:225-232.) Alternatively, CYSKP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide
5 synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of CYSKP, or any part thereof, may be altered during direct synthesis and/or combined with sequences
10 from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing.
15 (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active CYSKP, the nucleotide sequences encoding CYSKP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and
20 inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding CYSKP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CYSKP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding CYSKP and its initiation codon and upstream regulatory sequences are inserted
25 into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers
30 appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding CYSKP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in

vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences
 5 encoding CYSKP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or
 10 animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and
 15 Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al.
 20 (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding CYSKP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding CYSKP can be achieved using a
 25 multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSFORT1 plasmid (Life Technologies). Ligation of sequences encoding CYSKP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested
 30 deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of CYSKP are needed, e.g. for the production of antibodies, vectors which direct high level expression of CYSKP may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of CYSKP. A number of vectors

containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra;

- 5 Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; and Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184.)

- Plant systems may also be used for expression of CYSKP. Transcription of sequences encoding CYSKP may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, 15 New York NY, pp. 191-196.)

- In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding CYSKP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain 20 infective virus which expresses CYSKP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

- Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of 25 DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.)

- For long term production of recombinant proteins in mammalian systems, stable expression of CYSKP in cell lines is preferred. For example, sequences encoding CYSKP can be transformed into 30 cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the

introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; 5 Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) 10 Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. 15 These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the 20 sequence encoding CYSKP is inserted within a marker gene sequence, transformed cells containing sequences encoding CYSKP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding CYSKP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

25 In general, host cells that contain the nucleic acid sequence encoding CYSKP and that express CYSKP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

30 Immunological methods for detecting and measuring the expression of CYSKP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on CYSKP is preferred, but a competitive binding

assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

5 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding CYSKP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding CYSKP, or any fragments thereof, may be cloned into a vector
10 for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease
15 of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding CYSKP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence
20 and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CYSKP may be designed to contain signal sequences which direct secretion of CYSKP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the
25 polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture
30 Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding CYSKP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric CYSKP protein

containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of CYSKP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose
5 binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion
10 proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the CYSKP encoding sequence and the heterologous protein sequence, so that CYSKP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

15 In a further embodiment of the invention, synthesis of radiolabeled CYSKP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

20 CYSKP of the present invention or fragments thereof may be used to screen for compounds that specifically bind to CYSKP. At least one and up to a plurality of test compounds may be screened for specific binding to CYSKP. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of
25 CYSKP, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which CYSKP binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for
30 these compounds involves producing appropriate cells which express CYSKP, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing CYSKP or cell membrane fractions which contain CYSKP are then contacted with a test compound and binding, stimulation, or inhibition of activity of either CYSKP or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with CYSKP, either in solution or affixed to a solid support, and detecting the binding of CYSKP to the compound.

- 5 Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

CYSKP of the present invention or fragments thereof may be used to screen for compounds
10 that modulate the activity of CYSKP. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for CYSKP activity, wherein CYSKP is combined with at least one test compound, and the activity of CYSKP in the presence of a test compound is compared with the activity of CYSKP in the absence of the test compound. A change in the activity of CYSKP in the presence of the test compound is
15 indicative of a compound that modulates the activity of CYSKP. Alternatively, a test compound is combined with an in vitro or cell-free system comprising CYSKP under conditions suitable for CYSKP activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of CYSKP may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

- 20 In another embodiment, polynucleotides encoding CYSKP or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo
25 and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D.
30 (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding CYSKP may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding CYSKP can also be used to create “knockin” humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding CYSKP is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress CYSKP, e.g., by secreting CYSKP in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of CYSKP and cytoskeleton-associated proteins. In addition, the expression of CYSKP is closely associated with lung, reproductive (including placenta), neural (including brain), adrenal, endothelial, kidney, and spleen tissue, as well as with ovarian, breast, and testicular tumor tissue. Therefore, CYSKP appears to play a role in cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders. In the treatment of disorders associated with increased CYSKP expression or activity, it is desirable to decrease the expression or activity of CYSKP. In the treatment of disorders associated with decreased CYSKP expression or activity, it is desirable to increase the expression or activity of CYSKP.

Therefore, in one embodiment, CYSKP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory

- distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with
- 5 lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus,
- 10 systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a vesicle trafficking disorder such as cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes mellitus, diabetes insipidus, hyper- and hypoglycemia, Grave's disease, goiter, Cushing's disease, and Addison's disease,
- 15 gastrointestinal disorders including ulcerative colitis, gastric and duodenal ulcers, other conditions associated with abnormal vesicle trafficking, including acquired immunodeficiency syndrome (AIDS), allergies including hay fever, asthma, and urticaria (hives), autoimmune hemolytic anemia, proliferative glomerulonephritis, inflammatory bowel disease, multiple sclerosis, myasthenia gravis, rheumatoid and osteoarthritis, scleroderma, Chediak-Higashi and Sjogren's syndromes, systemic lupus erythematosus,
- 20 toxic shock syndrome, traumatic tissue damage, and viral, bacterial, fungal, helminthic, and protozoal infections; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and
- 25 other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal
- 30 syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety,

and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a cell motility disorder such as ankylosing spondylitis, Chediak-Higashi syndrome, Duchenne
5 and Becker muscular dystrophy, intrahepatic cholestasis, myocardial hyperplasia, cardiomyopathy, early onset peridontitis, cancers such as adenocarcinoma, ovarian carcinoma, and chronic myelogenous leukemia, and bacterial and helminthic infections; a reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian
10 hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, ectopic pregnancy, teratogenesis, cancer of the breast, fibrocystic breast disease, galactorrhea, a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, gynecomastia, hypergonadotropic and hypogonadotropic hypogonadism, pseudohermaphroditism,
15 azoospermia, premature ovarian failure, acrosin deficiency, delayed puberty, retrograde ejaculation and anejaculation, haemangioblastomas, cystsphaeochromocytomas, paraganglioma, cystadenomas of the epididymis, and endolymphatic sac tumours; and a muscle disorder such as myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis,
20 polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, and ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia.

25 In another embodiment, a vector capable of expressing CYSKP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified CYSKP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a
30 disorder associated with decreased expression or activity of CYSKP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of CYSKP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CYSKP including, but not limited to, those listed above.

In a further embodiment, an antagonist of CYSKP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CYSKP. Examples of such disorders include, but are not limited to, those cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive, and muscle disorders described above. In one aspect, an antibody which specifically binds CYSKP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express CYSKP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding CYSKP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CYSKP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of CYSKP may be produced using methods which are generally known in the art. In particular, purified CYSKP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind CYSKP. Antibodies to CYSKP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with CYSKP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to CYSKP have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or

fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of CYSKP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to CYSKP may be prepared using any technique which provides for the
5 production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

10 In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda, S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single
15 chain antibodies may be adapted, using methods known in the art, to produce CYSKP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) *Proc. Natl. Acad. Sci. USA* 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population
20 or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for CYSKP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin
25 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
30 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between CYSKP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering CYSKP epitopes is generally used, but a competitive binding assay may also be

employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for CYSKP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of CYSKP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple CYSKP epitopes, represents the average affinity, or avidity, of the antibodies for CYSKP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular CYSKP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the CYSKP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of CYSKP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of CYSKP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding CYSKP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding CYSKP. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding CYSKP. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995)

9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding CYSKP may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in CYSKP expression or regulation causes disease, the expression of CYSKP from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in CYSKP are treated by constructing mammalian expression vectors encoding CYSKP and introducing these vectors by mechanical means into CYSKP-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of CYSKP include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). CYSKP may be expressed

5 using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the

10 ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. *supra*)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding CYSKP from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID

15 TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these

20 standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to CYSKP expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding CYSKP under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive

25 element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for

30 receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a

method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference.

Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding CYSKP to cells which have one or more genetic abnormalities with respect to the expression of CYSKP. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding CYSKP to target cells which have one or more genetic abnormalities with respect to the expression of CYSKP. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing CYSKP to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary

skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding CYSKP to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for CYSKP into the alphavirus genome in place of the capsid-coding region results in the production of a large number of CYSKP-coding RNAs and the synthesis of high levels of CYSKP in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of CYSKP into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding CYSKP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by

scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding CYSKP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding CYSKP. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased CYSKP expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding CYSKP may be therapeutically useful, and in the treatment of disorders associated with decreased CYSKP expression or activity, a compound which specifically promotes expression of the polynucleotide encoding CYSKP may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in

altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound
5 based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding CYSKP is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding CYSKP are assayed
10 by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding CYSKP. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide
15 exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a
20 combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

25 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat.
30 Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

35 An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient.

Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of CYSKP, antibodies to CYSKP, and mimetics, agonists, antagonists, or inhibitors of CYSKP.

- 5 The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form.

- 10 These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

- 20 Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising CYSKP or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, CYSKP or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

- For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.
- 30

A therapeutically effective dose refers to that amount of active ingredient, for example CYSKP or fragments thereof, antibodies of CYSKP, and agonists, antagonists or inhibitors of CYSKP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by

- standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.
- 10 The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy.
- 15 Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art.

- 20 Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

- In another embodiment, antibodies which specifically bind CYSKP may be used for the diagnosis of disorders characterized by expression of CYSKP, or in assays to monitor patients being treated with CYSKP or agonists, antagonists, or inhibitors of CYSKP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for CYSKP include methods which utilize the antibody and a label to detect CYSKP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.
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- 30

A variety of protocols for measuring CYSKP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of CYSKP expression. Normal or standard values for CYSKP expression are established by combining body fluids or cell extracts

taken from normal mammalian subjects, for example, human subjects, with antibodies to CYSKP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of CYSKP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values.

- 5 Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding CYSKP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of CYSKP may be correlated with
10 disease. The diagnostic assay may be used to determine absence, presence, and excess expression of CYSKP, and to monitor regulation of CYSKP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding CYSKP or closely related molecules may be used to identify nucleic acid sequences which encode CYSKP. The specificity of the probe, whether it is made
15 from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding CYSKP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50%
20 sequence identity to any of the CYSKP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:35-68 or from genomic sequences including promoters, enhancers, and introns of the CYSKP gene.

Means for producing specific hybridization probes for DNAs encoding CYSKP include the cloning of polynucleotide sequences encoding CYSKP or CYSKP derivatives into vectors for the
25 production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

30 Polynucleotide sequences encoding CYSKP may be used for the diagnosis of disorders associated with expression of CYSKP. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including

adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with

5 lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus,

10 systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a vesicle trafficking disorder such as cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes mellitus, diabetes insipidus, hyper- and hypoglycemia, Grave's disease, goiter, Cushing's disease, and Addison's disease,

20 gastrointestinal disorders including ulcerative colitis, gastric and duodenal ulcers, other conditions associated with abnormal vesicle trafficking, including acquired immunodeficiency syndrome (AIDS), allergies including hay fever, asthma, and urticaria (hives), autoimmune hemolytic anemia, proliferative glomerulonephritis, inflammatory bowel disease, multiple sclerosis, myasthenia gravis, rheumatoid and osteoarthritis, scleroderma, Chediak-Higashi and Sjogren's syndromes, systemic lupus erythematosus,

25 toxic shock syndrome, traumatic tissue damage, and viral, bacterial, fungal, helminthic, and protozoal infections; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and

30 other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal

syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; a cell motility disorder such as ankylosing spondylitis, Chediak-Higashi syndrome, Duchenne and Becker muscular dystrophy, intrahepatic cholestasis, myocardial hyperplasia, cardiomyopathy, early onset periodontitis, cancers such as adenocarcinoma, ovarian carcinoma, and chronic myelogenous leukemia, and bacterial and helminthic infections; a reproductive disorder such as a disorder of prolactin production, infertility, including tubal disease, ovulatory defects, endometriosis, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, ectopic pregnancy, teratogenesis, cancer of the breast, fibrocystic breast disease, galactorrhea, a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, gynecomastia, hypergonadotropic and hypogonadotropic hypogonadism, pseudohermaphroditism, azoospermia, premature ovarian failure, acrosin deficiency, delayed puberty, retrograde ejaculation and anejaculation, haemangioblastomas, cystsphaeochromocytomas, paraganglioma, cystadenomas of the epididymis, and endolymphatic sac tumours; and a muscle disorder such as myocarditis, Duchenne's muscular dystrophy, Becker's muscular dystrophy, myotonic dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, infectious myositis, polymyositis, dermatomyositis, inclusion body myositis, thyrotoxic myopathy, and ethanol myopathy, angina, anaphylactic shock, arrhythmias, asthma, cardiovascular shock, Cushing's syndrome, hypertension, hypoglycemia, myocardial infarction, migraine, and pheochromocytoma, and myopathies including cardiomyopathy, encephalopathy, epilepsy, Kearns-Sayre syndrome, lactic acidosis, myoclonic disorder, and ophthalmoplegia. The polynucleotide sequences encoding CYSKP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered CYSKP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding CYSKP may be useful in assays that

detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding CYSKP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding CYSKP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of CYSKP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding CYSKP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding CYSKP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding CYSKP, or a fragment of a polynucleotide complementary to the polynucleotide encoding CYSKP, and will be employed under optimized conditions for identification of a specific gene or condition.

Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding CYSKP may be used to detect single nucleotide polymorphisms (SNPs). SNPs are
5 substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding CYSKP are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal
10 tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP
15 (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high
20 throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of CYSKP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be
25 accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray
30 can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the

activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

5 In another embodiment, CYSKP, fragments of CYSKP, or antibodies specific for CYSKP may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of
10 gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of
15 transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies,
20 or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental
25 compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties.
30 These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data

after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released
5 February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated
10 biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

15 Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given
20 conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are
25 visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein
30 spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for CYSKP to quantify the levels of CYSKP expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; 5 Mendozze, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation 10 between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

15 In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound 20 in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized 25 by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci.* 30 USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding CYSKP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding CYSKP on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, CYSKP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a

solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between CYSKP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with CYSKP, or fragments thereof, and washed. Bound CYSKP is then detected by methods well known in the art. Purified CYSKP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding CYSKP specifically compete with a test compound for binding CYSKP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with CYSKP.

In additional embodiments, the nucleotide sequences which encode CYSKP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/201,960, U.S. Ser. No. 60/202,729, U.S. Ser. No. 60/209,705, U.S. Ser. No. 60/210,149, and U.S. Ser. No. 60/213,215, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

Incye cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incye Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized

and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)⁺ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using
5 PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation
10 such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).
15 Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997,
20 supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA
25 sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.) The queries were
30 performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages

were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently

5 analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using

MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are

10 generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold

15 parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity

20 between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:35-68. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

25 IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative cytoskeleton-associated proteins were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin

30 (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode cytoskeleton-associated proteins, the encoded polypeptides were analyzed by querying

against PFAM models for cytoskeleton-associated proteins. Potential cytoskeleton-associated proteins were also identified by homology to Incyte cDNA sequences that had been annotated as cytoskeleton-associated proteins. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpr public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpr public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

"Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of CYSKP Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:35-68 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:35-68 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

In this manner, SEQ ID NO:44 was mapped to chromosome 17 within the interval from

62.90 to 64.20 centiMorgans, SEQ ID NO:49 was mapped to chromosome 14 within the interval from 73.70 to 76.40 centiMorgans, SEQ ID NO:50 was mapped to chromosome 8 within the interval from 25.80 to 40.30 centiMorgans, SEQ ID NO:54 was mapped to chromosome 1 within the interval from 117.6 to 132.4 centiMorgans, SEQ ID NO:64 was mapped to chromosome 4 within the interval
 5 from 56.7 to 60.5 centiMorgans, and SEQ ID NO:65 was mapped to chromosome 5 within the interval from 141.40 to 142.60 centiMorgans.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a
 10 particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel (1995) supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer
 15 search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

20

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by
 25 assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter
 30 of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding CYSKP are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled,

at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding CYSKP. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of CYSKP Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II
5 (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and
10 sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs,
15 and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1:
20 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC
25 DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

30 IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:35-68 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National

Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, *supra*), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), *supra*). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Skena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on

the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in
5 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with
10 an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
20 containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477,
25 Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a
30 cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different
35 fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially

expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC
5 computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

10 A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

15 Sequences complementary to the CYSKP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring CYSKP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of CYSKP. To inhibit transcription, a
20 complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the CYSKP-encoding transcript.

XII. Expression of CYSKP

Expression and purification of CYSKP is achieved using bacterial or virus-based expression
25 systems. For expression of CYSKP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3).

30 Antibiotic resistant bacteria express CYSKP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of CYSKP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding CYSKP by either homologous recombination or bacterial-mediated

transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect *Spodoptera frugiperda* (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, CYSKP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from *Schistosoma japonicum*, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from CYSKP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, *supra*, ch. 10 and 16). Purified CYSKP obtained by these methods can be used directly in the assays shown in Examples XVI and XVII, where applicable.

XIII. Functional Assays

CYSKP function is assessed by expressing the sequences encoding CYSKP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in

cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated
5 Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of CYSKP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding CYSKP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human
10 immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding CYSKP and other genes of interest can be analyzed by northern analysis or microarray techniques.

15 **XIV. Production of CYSKP Specific Antibodies**

CYSKP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the CYSKP amino acid sequence is analyzed using LASERGENE software
20 (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A
25 peptide synthesizer (Applied Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-CYSKP activity by, for example, binding the peptide or CYSKP to a substrate, blocking with
30 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring CYSKP Using Specific Antibodies

Naturally occurring or recombinant CYSKP is substantially purified by immunoaffinity chromatography using antibodies specific for CYSKP. An immunoaffinity column is constructed by covalently coupling anti-CYSKP antibody to an activated chromatographic resin, such as

CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing CYSKP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of CYSKP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/CYSKP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and CYSKP is collected.

XVI. Identification of Molecules Which Interact with CYSKP

CYSKP, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled CYSKP, washed, and any wells with labeled CYSKP complex are assayed. Data obtained using different concentrations of CYSKP are used to calculate values for the number, affinity, and association of CYSKP with the candidate molecules.

Alternatively, molecules interacting with CYSKP are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) *Nature* 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

CYSKP may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of CYSKP Activity

A microtubule motility assay for CYSKP measures motor protein activity. In this assay, recombinant CYSKP is immobilized onto a glass slide or similar substrate. Taxol-stabilized bovine brain microtubules (commercially available) in a solution containing ATP and cytosolic extract are perfused onto the slide. Movement of microtubules as driven by CYSKP motor activity can be visualized and quantified using video-enhanced light microscopy and image analysis techniques. CYSKP activity is directly proportional to the frequency and velocity of microtubule movement.

Alternatively, an assay for CYSKP measures the formation of protein filaments in vitro. A solution of CYSKP at a concentration greater than the "critical concentration" for polymer assembly is applied to carbon-coated grids. Appropriate nucleation sites may be supplied in the solution. The grids are negative stained with 0.7% (w/v) aqueous uranyl acetate and examined by electron microscopy. The appearance of filaments of approximately 25 nm (microtubules), 8 nm (actin), or 10 nm (intermediate filaments) is a demonstration of protein activity.

Alternatively, an assay for CYSKP measures the binding affinity of CYSKP for actin as described by Hammell, R.L. and Hitchcock-DeGregori, S.E. (1997, J. Biol. Chem. 272:22409-22416). CYSKP and actin are prepared from in vitro recombinant cDNA expression systems and the N-terminus of CYSKP is acetylated using methods well known in the art. Binding of N-terminal acetyl-
5 CYSKP to actin is measured by cosedimentation at 25 °C in a Beckman model TL-100 centrifuge as described. The bound and free CYSKP are determined by quantitative densitometry of SDS-polyacrylamide gels stained with Coomassie Blue. Apparent binding constants (K_{app}) and Hill coefficients (H) are determined by using methods well known in the art to fit the data to the equation as described by Hammell and Hitchcock-DeGregori (1997, supra). The CYSKP:actin ratio, determined
10 using densitometry, is normalized. Hammell and Hitchcock-DeGregori (1997, supra) have shown that saturation of binding corresponds to a CYSKP:actin molar ratio of 0.14, a stoichiometry of 1 CYSKP:7 actin. The binding of CYSKP to actin is proportional to the CYSKP activity.

Alternatively, CYSKP activity is measured as ability to bind to microtubules. Microtubules are purified from adult rat brain by reversible assembly (Vallee, R. B. (1982) Methods Enzymol.
15 134:89-104) or the taxol method (Vallee, R. B. (1982) J. Cell Biol. 92:435-442) using PEM buffer (100 mM PIPES, pH 6.6, 1mM EGTA, 1mM $MgSO_4$). To separate the MAPs from tubulin, the pellets from twice-cycled microtubules are resuspended in PEM buffer and applied to a 0.1 M $MgSO_4$ -saturated phosphocellulose column as described by Sloboda, R. D. and Rosenbaum, J. L. ((1982) Methods Enzymol. 85:409-416). The fractions containing protein are applied to a second
20 phosphocellulose column. In a total volume of 100 ml, 20 ml of CYSKP (250 mg/ml) is added to 80 ml of whole microtubules (450 mg/ml) or tubulin (300 mg/ml) and incubated at 37 °C for 10 minutes in the presence of 1 mM GTP and 50 mM taxol. The suspension is centrifuged, the supernatant is removed, and the microtubule pellet is resuspended to the original reaction volume in PEM buffer. To assess the partitioning of CYSKP between the supernatant and pellet fractions, equal amounts of supernatant and
25 resuspended pellet are placed in SDS sample buffer and assayed on a 5-20% gradient SDS polyacrylamide gel stained with Coomassie Brilliant Blue. The amount of CYSKP in the pellet fraction is proportional to the binding of CYSKP to microtubules.

Alternatively, CYSKP activity is associated with its ability to form protein-protein complexes and is measured by its ability to regulate growth characteristics of NIH3T3 mouse fibroblast cells. A
30 cDNA encoding CYSKP is subcloned into an appropriate eukaryotic expression vector. This vector is transfected into NIH3T3 cells using methods known in the art. Transfected cells are compared with non-transfected cells for the following quantifiable properties: growth in culture to high density, reduced attachment of cells to the substrate, altered cell morphology, and ability to induce tumors when injected into immunodeficient mice. The activity of CYSKP is proportional to the extent of increased growth or

frequency of altered cell morphology in NIH3T3 cells transfected with CYSKP.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention.

- 5 Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
1889577	1	1889577CD1	35	1889577CB1
2427982	2	2427982CD1	36	2427982CB1
2470833	3	2470833CD1	37	2470833CB1
2080579	4	2080579CD1	38	2080579CB1
2156553	5	2156553CD1	39	2156553CB1
2182855	6	2182855CD1	40	2182855CB1
2242106	7	2242106CD1	41	2242106CB1
2726877	8	2726877CD1	42	2726877CB1
2738233	9	2738233CD1	43	2738233CB1
1833116	10	1833116CD1	44	1833116CB1
001799	11	001799CD1	45	001799CB1
119814	12	119814CD1	46	119814CB1
1295420	13	1295420CD1	47	1295420CB1
1309364	14	1309364CD1	48	1309364CB1
1315267	15	1315267CD1	49	1315267CB1
1403289	16	1403289CD1	50	1403289CB1
1607607	17	1607607CD1	51	1607607CB1
1660025	18	1660025CD1	52	1660025CB1
1796836	19	1796836CD1	53	1796836CB1
2880670	20	2880670CD1	54	2880670CB1
2913976	21	2913976CD1	55	2913976CB1
3092084	22	3092084CD1	56	3092084CB1
3882482	23	3882482CD1	57	3882482CB1
4933451	24	4933451CD1	58	4933451CB1
5043904	25	5043904CD1	59	5043904CB1
5202390	26	5202390CD1	60	5202390CB1
5526375	27	5526375CD1	61	5526375CB1
5677408	28	5677408CD1	62	5677408CB1
5982278	29	5982278CD1	63	5982278CB1
6437362	30	6437362CD1	64	6437362CB1
4173970	31	4173970CD1	65	4173970CB1
2772751	32	2772751CD1	66	2772751CB1
2793768	33	2793768CD1	67	2793768CB1
3035248	34	3035248CD1	68	3035248CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	1889577CD1	g3347848	0.00E+00	kinesin light chain 2 [Mus musculus]
2	2427982CD1	g2760161	3.00E-64	outer arm dynein light chain 2 [Anthracidaris crassispina]
3	2470833CD1	g11094032	1.00E-147	[Mus musculus] (AF312712) gamma-parvin
4	2080579CD1	g11036542	0	[Homo sapiens] (AF237772) gamma-parvin
		g6141549	2.50E-101	JNK/SAPK-associated protein-1 (JIP-1) scaffold protein [Mus musculus] (Meyer, D. et al. (1999) J. Biol. Chem. 574:35113-35118)
5	2156553CD1	g5419859	2.00E-170	hypothetical protein similar to tubulin- tyrosine ligase [Homo sapiens] (Lafanechere, L. et al. (1998) J. Cell Sci. 11:171-181)
6	2182855CD1	g2276319	0	axonemal dynein heavy chain [Homo sapiens]
7	2242106CD1	g3834443	2.00E-13	[Drosophila melanogaster] cytoplasmic dynein intermediate chain isoform DIC5b
8	2726877CD1	g118156	1.20E-10	70kD dynein intermediate chain [Chlamydomonas reinhardtii]
		g4778	1.30E-12	Uso1 protein [Saccharomyces cerevisiae] (Nakajima, H. et al. (1991) J. Cell Biol. 113:245-260)
9	2738233CD1	g4185884	7.70E-33	Groovin (Kakapo) [Drosophila melanogaster] (Strumpf, D. and T. Volk (1998) J. Cell Biol. 143:1259-1270)
10	1833116CD1	g10880797	0	[Mus musculus] Syne-1A
		g12082089	0	[Homo sapiens] hARPX
		g12082091	0	[Gallus gallus] GARPX
11	1799CD1	g3283070	1.70E-07	p80 katanin [Xenopus laevis] (McNally, F.J., Thomas, S. (1998) Mol. Biol. Cell 9:1847- 1861)
		g3005599	5.00E-09	[Homo sapiens] (AF052432) katanin p80 subunit
12	119814CD1	g3243131	4.40E-18	titin [Drosophila melanogaster] (Machado, C. et al. (1998) J. Cell Biol. 141:321-333)
		g5870837	1.00E-113	[Homo sapiens] titin-like protein
13	1295420CD1	g180622	5.60E-37	cytoplasmic linker protein-170 alpha-2 [Homo sapiens] (Pierre, P. et al. (1992) Cell 70:887-900)
14	1309364CD1	g12667401	0	[Homo sapiens] NUF2R
		g12667403	0	[Mus musculus] NUF2R

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
15	1315267CD1	g53996	8.00E-74	Tcp-10 (transmission control protein) [Mus musculus] (Davies, P. et al. (1991) Mann. Genome 1:235-241)
16	1403289CD1	g5733814	4.60E-196	angiotensin II AT2 receptor-interacting protein (Bedecs, K. et al. (1997) Biochem. J. 325:449-454)
17	1607607CD1	g3158498	1.60E-19	Contains similarity to Pfam domain: PF00628 (PHD finger) (Aasland, R. et al. (1995) Trends Biochem. Sci. 20:56-59)
18	1660025CD1	g3253105	9.80E-20	[Caenorhabditis elegans] strong similarity to the SNF2/RAD54 family of helicases (Eisen, J. et al. (1995) Nucleic Acids Res. 23:2715-2723)
19	1796836CD1	g414111	7.20E-14	class II INCENP protein (inner centromere protein) [Gallus gallus] (Mackay, A. et al. (1993) J. Cell Biol. 123:373-385)
20	2880670CD1	g1813638	6.90E-16	PF20 [Chlamydomonas reinhardtii] (Smith, E. and P. Lefebvre (1997) Mol. Biol. Cell 8:455-457)
21	2913976CD1	g63898	3.10E-56	Zyxin [Gallus gallus] (Sadler, I. et al. (1992) J. Cell Biol. 119:1573-1587)
22	3092084CD1	g1154645	2.30E-10	head-elevated expression in 0.9 kb [Drosophila melanogaster] (Yang, M.Y. et al. (2000) Genetics 154:285-297)
23	3882482CD1	g5825592	7.60E-171	katanin p60 [Xenopus laevis]
24	4933451CD1	g684936	3.20E-30	peptide with resemblance to the actin family [Homo sapiens]
25	5043904CD1	g2832237	2.10E-06	cep250 centrosome associated protein [Homo sapiens] (Mack, G.J. et al. (1998) Arthritis Rheum. 41:551-558)
26	5202390CD1	g6572155	2.90E-21	[Homo sapiens] dj1014D13.2 (novel protein similar to ACTN3 (actinin, alpha 3))
27	5526375CD1	g2443272	2.80E-77	motor domain of KIF12 [Mus musculus] (Nakagawa, T. et al. (1997) Proc. Natl. Acad. Sci. USA 94:9654-9659)
28	5677408CD1	g6651427	2.20E-05	dynein light intermediate chain 1 (LIC-2) [Rattus norvegicus] (Hughes, S.M. et al. (1995) J. Cell Sci. 108:17-24)
29	5982278CD1	g6006743	0	mitotic kinesin-like protein 1 [Danio rerio]
		g6723675	0	[Homo sapiens] mitotic kinase-like protein-1

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
30	6437362CD1	g4929268	2.00E-38	LOMP protein (LIM and PDZ domain protein) [Homo sapiens]
31	4173970CD1	g3879121	1.10E-146	predicted using Genefinder; Similarity to Mouse ankyrin [Caenorhabditis elegans]
32	2772751CD1	g4545313	7.00E-103	[Mus musculus] prominin-like protein (Corbeil, D. et al. (2000) J. Biol. Chem. 275:5512-5520)
33	2793768CD1	g485107	2.70E-85	weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7
34	3035248CD1	g1333846	8.20E-45	intermediate filament associated protein [Cricetulus griseus] (Skalli, O. et al. (1994) J. Cell Biol. 125:159-170)

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	1889577CD1	622	T30 S90 T451 S499 S507 S539 T568 S615 Y345 Y431 S428 S557 S581 S619 S13 S151 T163 S232 T470 S507 S519 S521 T568 S589 S610	N449 N587	Kinesin light chain repeat BL01160:V88-S141, G191-P237, D238-A266, L267-C305, A308-R348, R349-C375, Q379-E420, E433-K480, L12-P50 KINESIN LIGHT CHAIN SIGNATURE PR00381:A97-A114, G191-S210, R213-T231, H278-R295, D322-E342, R357-K378 KINESIN LIGHT CHAIN PROTEIN KLC MOTOR MICROTUBULES COILED COIL REPEAT PD012762:L12-Q174 KINESIN LIGHT CHAIN REPEAT DM01439 A41539 1-234:M1-L220 signal_cleavage:M1-P50 Kinesin light chain repeat Kinesin2:Q223-N264, D265-K306 Kinesin light chain repeat Kinesin Light:Q223-N264 D265-K306 Leucine Rich Repeat LRR:N49-K70, N 71-G92, T94-K115, K116-P140 COSMID C06A8 PROTEIN T09A5.9 CHROMOSOME III LEUCINEREPEAT REPEAT PD035408:S54-T179 Leucine Rich Repeat signature PR00019:L69-I82	BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO SPScan HMMER-PFAM MOTIFS HMMER-PFAM BLAST-PRODOM BLIMPS-PRINTS HMMER-PFAM
2	2427982CD1	190	T6 T94 T6 T167			
3	2470833CD1	331	S37 S67 T188 S267 S293 T36 S37 S101 S169 S176 T188 T305 T317	N55 N114 N274	Calponin homology (CH) domain CH:N210-T317	HMMER-PFAM
4	2080579CD1	239	T92 S148 T174 S191 S266			MOTIFS
5	2156553CD1	488	S237 T370 T402 T121 T226 S428	N167 N168	PROTEIN CHROMOSOME TUBULIN TYROSINE LIGASE TTL C55A6.2 ZK1128.6 III PD008766:G63-V285	BLAST-PRODOM

Table 3 (cont.)

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6	2182855CD1	1190	S26 S197 S207 S312 T354 S356 S492 S509 S519 S593 S686 T902 S920 S976 T992 Y811 Y955 T45 T98 S149 T163 T233 T350 S406 T446 S468 S524 S896 S976 S15 S56 S168 S189 S203 T240 S77 T213	N20 N23 N156 N308 N433 N548 N635 N777	PROTEIN DYNEIN CHAIN MOTOR MICROTUBULES ATPBINDING HEPTAD REPEAT PATTERN HEAVY PD003982.S920-V1190 Go DYNEIN; HEAVY; CILIARY; CYTOSOLIC DM04585 P39057 2948-4465:L14-V1190 G_Beta_Repeats:L130-N144	BLAST-PRODOM BLAST-DOMO MOTIFS
7	2242106CD1	270	S15 S56 S168 S189 S203 T240 S77 T213		signal_cleavage:M1-T25 transmem_domain:V29-L53 WD domain, G-beta repeat WD40:A116-S155, T207-Q245	SPScan HMMER HMMER-PFAM
8	2726877CD1	647	S38 T173 T184 S322 S442 T483 T503 S510 S589 T14 S122 T134 T189 T408 S447 S461 S472 S510 S579 S593	N99 N120 N316 N480 N508 N644	PROTEIN COILED COIL CHAIN MYOSIN REPEAT HEAVY ATPBINDING FILAMENT HEPTAD PD000002:Q409-E619	BLAST-PRODOM
9	2738233CD1	1086	T386 S12 S32 T86 S142 T251 S298 T343 T404 T414 T421 S427 S512 S559 S594 S618 T651 S671 T748 T799 S825 S870 S900 S954 S962 S963 Y146 S58 S75 S185 T286 S307 S366 T404 S512 S556 S559 S658 S675 S977 T987	N182 N359 N545	Spectrin repeat:R2-B66, N69-E171, V174-E285, R288-H394, G397-R501, T699-Q726, Q729-D836 Spectrin repeat proteins PF00435:W155-K170	HMMER-PFAM BLIMPS-PFAM
10	1833116CD1	396	S104 S108 T341 T343 S367 T378 S388 T34 S163 S189 T243 S258	N21 N101	P59-K245, Q266-D395 Actin T3-L37, Q73-A127, R137-R191, I289-T343, D346-D395 Actins V333-K393 Actins signatures L4-I289 ACTINS AND ACTIN-RELATED PROTEINS Q266-K393 ACTIN	HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN BLAST_DOMO BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
11	001799CD1	304	Y121 Y183 T33 S43 T58 S137 S254 S30 S89 S176 S131 S229 S255	N31 N52 N124	W172-D189 Aldehyde dehydrogenases motif V147-W249 P-value 5.9e-07 KATANIN P80 centrosome-binding subunit	BLIMPS_BLOCKS BLAST_PRODUM
12	119814CD1	201	T139 Y24 S4 S60 S68 T96 T106 T144	N148	M1-A23 signal cleavage G66-T125, S10-A28 Immunoglobulin domain	SPSCAN HMMER_PFAM
13	1295420CD1	547	T399T2 T58 T77 T192 T260 S491 T518 T154 T309 T374 T377 T386 T454 T515 T518	N190	G314-F345 G436-F467 Cap_Gly G314-S356, G436-P478 CAP-Gly domain T117-R158, T160-S191, N197-R229 Ank repeat G321-F345 CAP-Gly domain proteins G436-F476 MICROTUBULES CYTOSKELETON COILED COIL	MOTIFS HMMER_PFAM HMMER_PFAM BLIMPS_BLOCKS BLAST_PRODUM
14	1309364CD1	464	Y369 Y445 S118 T117 S217 T220 S232 S239 S340 T24 T32 T90 T137 S147 S232 T372 T428	N30 N215	E417-P492, L294-K362 CAP (cytoskeleton-associated protein)-GLY DOMAIN Q177-K418 COILED COIL MYOSIN REPEAT	BLAST_DOMO BLAST_PRODUM
15	1315267CD1	569	S3 T68 S85 S103 T229 S306 S356 T408 T482 T535 S551 T246 S20 T29 T31 T146 S167 T217 S292 T318 S385 T450 T477	N46 N121 N155 N304 N406	I465-E475 Muscarinic M4 receptor signature H386-A524 TCOMPLEX Male germ-cell specific protein	BLIMPS_PFAM BLAST_PRODUM
16	1403289CD1	436	S4 T17 S111 T167 T212 S222 S255 S308 S407 S421 S434 T35 S390 T58 T76 T97 T139 T153 T187 S213 S220 S235 S249 S270 Y74	N80 N336	L254-L275 L306-L327 Leucine zipper K196-E395 COILED COIL MYOSIN REPEAT Q107-E395 TRICHOHYALIN (hair root sheath protein)	MOTIFS BLAST_PRODUM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	1607607CD1	363	S106 T206 T275 S288 S324 T331 T341 S51 T63 T162 S212 T336	N229 N307	L6-L27 L55-L76 Leucine Zipper L6-E16 Prepro orexin signature S3-E199 F33E11.3 PROTEIN similar to PHD finger K159-K165 Regulator of G protein signaling domain Q92-R103 5-hydroxytryptamine 2C receptor signature E60-P247 TOPOISOMERASE I DNA ISOMERASE REPEAT A17-S246 CYLICIN II sperm head cytoskeletal protein	MOTIFS BLIMPS_PRINTS BLAST_PRODROM BLIMPS_PPFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_DOMO
18	1660025CD1	247	S366 S45 S69 T96 S139 S148 S161 S183 S238 T264 T392 S416 Y399 S224 T264 T369 S381		Q133-K383 COILED COIL MYOSIN REPEAT Q135-Q412 TRICHOHYALIN (hair root sheath protein)	BLAST_PRODROM BLAST_DOMO
19	1796836CD1	441	S366 S45 S69 T96 S139 S148 S161 S183 S238 T264 T392 S416 Y399 S224 T369 S381	N113 N128	WDREPEAT PROTEIN PF20 REPEAT WD FLAGELLA PD134845: E51-A178 LIM domains: C22-E80; C82-A139; C142-A208 LIM domain BL00478: Y43-L57 LIM domain signatures: E3-Y75; Y63-R206; M1-K137 LIM METAL-BINDING REPEAT DM00055 Q04584 464-533: F134-H203 LIM domain motifs: C22-L57; C82-I115; C142-L181	BLAST-PRODROM BLAST_PRODROM BLAST_DOMO
20	2880670CD1	183	T48 S53 S68 T88	N66		BLAST-PRODROM
21	2913976CD1	212	S124 S143 T49 T52 Y75 Y172			HMMER-PFAM BLIMPS-BLOCKS PROFILESSCAN
22	3092084CD1	227	T11 S73 S56 S58 S113 S221 S6 T7 S46 T201 V141	N19	CALDESMON DM06224 P12957 1-755: T7-N197 (P-value = 7.6e-08)	BLAST-PRODROM BLAST_PRODROM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
23	3882482CD1	490	T318 S42 S71 S87 S143 T150 S174 T318 S416 S440 S448 T457 S473 S75 S145 T252 T278 S285 S314 S325 T382 Y377	N271	AAA ATP-binding protease domain: G243-R433 AAA-protein family protease signatures BL00674: W207-P227; W241-A262; S274-R316 G338-K384; G414-R433 KATANIN P60 SUBUNIT PD116869: M1-P135 AAA-PROTEIN FAMILY DM00024 P34808 188-348: D208-L368 AAA motif: V352-R370 ATP/GTP binding site (P-loop): G248-T255 Actin domain: M1-M114 Actins proteins signature BL00406: T5-K39 Actin signature PR00190: E24-V33 PROTEIN STRUCTURAL ACTIN MULTIGENE FAMILY ACETYLATION MUSCLE CYTOSKELETON CYTOPLASMIC ACTINLIKE PD000056: V6-L117 ACTINS AND ACTIN-RELATED PROTEINS DM00167 P20360 3-272: A2-M114 PROTEIN COILED COIL CHAIN MYOSIN REPEAT HEAVY ATPBINDING FILAMENT HEPTAD PD000002: L617-D679 (P-value = 2.5e-05) C2-DOMAIN DM00150 P24506 157-283: R460-S584 (P-value = 7.2e-06)	HMME-PFAM BLIMPS-BLOCKS BLAST-PRODOM BLAST-DOMO MOTIFS MOTIFS HMME-PFAM BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO
24	4933451CD1	133	S52 S115			
25	5043904CD1	912	T162 S592 S773 T28 S54 S63 S81 S135 S251 S260 S278 T239 T374 S383 S553 S565 T620 T636 S647 T690 S744 T786 S823 S830 S889 S908 S7 T50 S157 T192 S199 S243 T308 T326 S334 T542 T550 S576 S584 S640 T671 S752 S766 S774 S777 S780 T862 Y681	N483 N742		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
26	5202390CD1	1076	S602 S303 T10 T45 T176 S204 T206 S393 S422 S454 S469 T475 T492 S494 S509 S518 S575 S592 T630 S632 S657 S732 S748 T759 T776 S822 S828 S880 T954 S982 S22 S57 S140 S184 T185 S203 T238 S253 S273 S316 S406 T410 S505 S548 T606 S626 S647 T835 T842 T856 T885 T898 T950 Y149 Y198 Y733 Y918	N150 N289 N312 N405 N421 N462	Calponin homology (CH) domain: P288-S393 ALPHA-ACTININ ACTIN-BINDING DOMAIN DM00325 P18091 28-252: A290-L385	HMME-PFAM BLAST-DOMO
27	5526375CD1	542	S223 S113 S36 T80 S162 S280 S113 T158 S179 S218 S231 S272 T355 T366 S540	N188 N292	Kinesin motor domain: R31-N394 Kinesin motor domain BL00411: P25-E39; G100-G121; V157-L175 G216-L240; L264-L305; H314-P344 Kinesin motor domain signature: A247-A297 Kinesin heavy chain signatures PR00380: G100-G121; H225-I242; K263-R281; I315-T336 PROTEIN MOTOR ATPBINDING COILED COIL MICROTUBULES KINESINLIKE KINESIN MITOSIS HEAVY PD000458: R31-L401 KINESIN MOTOR DOMAIN DM00198 P46871 3-343: E23-Q370 ATP/GTP binding site (P-loop): G109-T116 Kinesin motor domain motif: G262-E273 ATP/GTP binding site (P-loop): G38-T45	HMME-PFAM BLIMPS-BLOCKS PROFILESCAN BLIMPS-PRINTS BLAST-PRODROM BLAST-DOMO MOTIFS MOTIFS MOTIFS
28	5677408CD1	351	S340 T5 S22 T77 S92 S136 S186 S221 S284 T304 T105 S196 T205 T220 S343 Y336	N20		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
29	5982278CD1	856	T13 S18 S807 S808 T84 S125 T200 S221 T266 S272 S334 T347 T369 T580 S710 T757 S763 T789 T823 S3 T8 S74 S116 S186 S187 S298 S341 T344 T366 T382 S605 T622 T563 T679 T793 S802	N48 N49 N345 N361 N565 N800	Kinesin motor domain: R31-E466 Kinesin motor domain BL00411: P25-D39; K69-Q85; G103-G124 G130-F140; Y216-L234; G283-I307 L333-L374; M385-P415 Kinesin motor domain signatures: D317-L364 Kinesin heavy chain signatures PR00380: G103-G124; T292-L309; Q332-E350; V386-V407 PROTEIN MOTOR MICROTUBULES ATPBINDING COILED COIL KINESIN LIKE SIMILAR MITOTIC PROTEIN1 PD013891: E664-L841 KINESIN MOTOR DOMAIN DM00198 Q02241 4-443: A4-I446 ATP/GTP binding site (P-loop): G112-T119 Kinesin motor domain motif: S331-E342 LIM domain: C986-S1049 Calponin family repeat BL01052: F44-I69 LIM domain: F1008-L1022 LIM domain signature: K964-S1047 Calponin signature PR00889: S25-F39; C55-L72 CALPONIN FAMILY REPEAT DM01491 P51911 6-147: P4-S116 LIM domain motif: C986-L1022	HMMER-PFAM BLIMPS-BLOCKS PROFILES SCAN BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO MOTIFS MOTIFS HMMER-PFAM BLIMPS-BLOCKS BLIMPS-BLOCKS PROFILES SCAN BLIMPS-PRINTS BLAST-DOMO MOTIFS
30	6437362CD1	1056	T164 S256 S377 S408 S979 S38 T46 S173 S231 S233 S327 T411 S435 T451 S511 S601 S637 S746 S836 S846 S897 S951 S972 S1027 T35 S109 T113 S120 S169 S185 S251 S373 S403 T529 T537 T553 T630 S647 S702 S710 S753 S889 S974 S981 Y179 Y294	N272 N275 N475 N609	Ank repeat: K347-N379; N77-K109; K110-E142; T144-V176; S177-G209; L212-E244; N246-K278; T279-V311; S314-K346 signal_cleavage: M1-A18 signal_peptide: M1-A18 transmembrane domain: V2-N22, V277-G296, L326-V344 AC133 ANTIGEN PROMININ HOMOLOG: M1-R333	HMMER-PFAM SPSCAN HMMER HMMER BLAST PRODOM
31	4173970CD1	1569				
32	2772751CD1	680	S113 S212 S340 S343 S357 T104 T159 T276 T328 T342	N210 N233 N251 N56 N66 N89		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
33	2793768CD1	590	S3 S373 S432 S461 S495 S499 S548 S56 S561 S586 S83 T199 T228 T234 T255 T286 T331 T354 T357 T433 T445 T454 T534 T547 T588	N101 N166 N233	signal_cleavage: M1-S56 Ankyrin repeat: R40-R72, Q73-T102 SIMILAR TO ANKYRIN REPEAT REGION OF FOWLPOX VIRUS BAMHIORF7 PROTEIN: W75-H284, G348-Y469	SPSCAN HMMER_PFAM BLAST_PRODOM
34	3035248CD1	315	S151 S291 T115 T207 T273		signal_cleavage: M1-G26 signal_peptide: M1-S24 transmembrane domain: P4-F20 INTERMEDIATE FILAMENT ASSOCIATED PROTEIN K147-T218 TROPOMYOSIN ALTERNATIVE SPLICING SIGNAL PRECURSOR CHAIN: E39-S213 INTERMEDIATE FILAMENT: K121-T218	SPSCAN HMMER HMMR BLAST_PRODOM BLAST_PRODOM BLAST_DOMO

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
35	1889577CB1	2345	902-952	3824958H1 (BRAXNOT01)	1	284
35	1889577CB1	2345		1915360R6 (PROSTUT04)	774	1278
35	1889577CB1	2345		1812980F6 (PROSTUT12)	102	646
35	1889577CB1	2345		3152565H1 (ADRENON04)	1799	2066
35	1889577CB1	2345		1369763H1 (BSTMN02)	1608	1840
35	1889577CB1	2345		1784544F6 (BRAINF01)	1873	2345
35	1889577CB1	2345		674685H1 (CRBLNOT01)	1516	1769
35	1889577CB1	2345		2838122F6 (DRGLNOT01)	1016	1563
35	1889577CB1	2345		1649402F6 (PROSTUT09)	384	896
36	2427982CB1	709		71263527V1	624	709
36	2427982CB1	709		71247061V1	1	683
37	2470833CB1	1569	1-721	1684180F6 (PROSN015)	1	497
37	2470833CB1	1569		868966R6 (LUNGAST01)	842	1407
37	2470833CB1	1569		3576193T6 (BRONNOT01)	980	1569
37	2470833CB1	1569		1534629F1 (SPLNNOT04)	677	1197
37	2470833CB1	1569		5296329H1 (COLENOT02)	493	730
37	2470833CB1	1569		1716065F6 (UCMCNOT02)	207	652
38	2080579CB1	1172	1-148, 686-854	868135H1 (BRAITUT03)	368	632
38	2080579CB1	1172		3458305F6 (293TF1T01)	1	433
38	2080579CB1	1172		2080579T6 (UTRSNOT08)	583	1143
38	2080579CB1	1172		2361824H1 (LUNGFT05)	939	1172
38	2080579CB1	1172		5174845H1 (EPIBTXT01)	442	637
39	2156553CB1	2380	1-360, 2126-2380, 1121-1655	5322363H1 (FIBPFEN06)	1	260
39	2156553CB1	2380		2916949T6 (THYMFET03)	1769	2380
39	2156553CB1	2380		866038X04D1 (BRAITUT03)	371	937
39	2156553CB1	2380		2916949F6 (THYMFET03)	1341	1886
39	2156553CB1	2380		2156553F6 (BRAINF09)	705	1224
39	2156553CB1	2380		1722673F6 (BLADNOT06)	1176	1582
39	2156553CB1	2380		4899945H1 (OVARBIT01)	245	531
39	2156553CB1	2380		1758833H1 (PITUNOT03)	236	485
40	2182855CB1	4396	2141-2667, 1- 1505, 1737- 1890, 3803- 4396	2816335F6 (BRSTNOT14)	3897	4396
40	2182855CB1	4396		2967273F6 (SCORNOT04)	580	1116

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
40	2182855CB1	4396		1611084F6 (COLINTUT06)	3554	3992
40	2182855CB1	4396		1785722H1 (BRAINOT10)	2610	2857
40	2182855CB1	4396		2182855F6 (SININOT01)	3389	3914
40	2182855CB1	4396		1484284F6 (CORPNOT02)	1	607
40	2182855CB1	4396		92276318	61	3799
40	2182855CB1	4396		2321435H1 (OVARNOT02)	2609	2794
40	2182855CB1	4396		1578313H1 (DUODNOT01)	1452	1546
40	2182855CB1	4396		1618459F6 (BRAITUT12)	2925	3464
40	2182855CB1	4396		2321435X308F1 (OVARNOT02)	1811	2391
41	2242106CB1	1831	1-509, 626-1018	965728R1 (BRSTNOT05)	1283	1831
41	2242106CB1	1831		1650350F6 (PROSTUT09)	322	1031
41	2242106CB1	1831		1396324T1 (THYRNUT03)	948	1660
41	2242106CB1	1831		6843794H1 (KIDNTMN03)	191	985
41	2242106CB1	1831		956964T1 (KIDNNOT05)	1019	1667
41	2242106CB1	1831		70846228V1	1	216
42	2726877CB1	3249	1979-2045, 2854-2873, 1857-1919, 2543-2608	3728286F6 (SMCCNON03)	1073	1504
42	2726877CB1	3249		3645568F6 (LJUNGNOT34)	383	933
42	2726877CB1	3249		4969912H1 (KIDEUNC10)	151	425
42	2726877CB1	3249		2500944T6 (ADRETUT05)	1254	1839
42	2726877CB1	3249		2726877F6 (OVARUT05)	1603	2060
42	2726877CB1	3249		4195125T6 (COLITUT02)	2652	3249
42	2726877CB1	3249		4972430H1 (HELATXT02)	901	1191
42	2726877CB1	3249		4195125F6 (COLITUT02)	2257	2810
42	2726877CB1	3249		5492146H1 (DRGTNON04)	2128	2380
42	2726877CB1	3249		3894803H1 (TLYMNUT05)	1	296
42	2726877CB1	3249		3728286T6 (SMCCNON03)	1682	2279
43	2738233CB1	4133	1-194, 4026-4133, 1607-2971, 3066-3186	1649466F6 (PROSTUT09)	2737	3394
43	2738233CB1	4133		2267313R6 (UTRSNOT02)	2211	2730
43	2738233CB1	4133		93882312_CD	126	3516
43	2738233CB1	4133		2945874H2 (BRAITUT23)	2710	3006
43	2738233CB1	4133		2242201F6 (PANCTUT02)	1538	2077

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
43	2738233CB1	4133		653470R6 (EOSINOT03)	685	1068
43	2738233CB1	4133		2267313T6 (UTRSNOT02)	3481	4109
43	2738233CB1	4133		2962383H1 (ADRENOT09)	1	277
43	2738233CB1	4133		1467024F6 (PANCTUT02)	1948	2420
43	2738233CB1	4133		3555108H1 (SYNONOT01)	1394	1704
43	2738233CB1	4133		2965786H1 (SCORNOT04)	217	469
43	2738233CB1	4133		1262951R1 (SYNORAT05)	3959	4133
43	2738233CB1	4133		1260043T1 (MENITUT03)	3370	4017
43	2738233CB1	4133		1486351H1 (CORPNOT02)	1236	1463
43	2738233CB1	4133		3765643F6 (BRSTNOT24)	277	758
44	1833116CB1	1754	1700-1754	2852676F6 (BRSTTUT13)	25	529
44	1833116CB1	1754		3128645H1 (LUNGTTUT12)	539	839
44	1833116CB1	1754		5016828H1 (BRAXNOT03)	632	886
44	1833116CB1	1754		413418R1 (BRSTNOT01)	979	1615
44	1833116CB1	1754		1442616R1 (THYRNOT03)	1247	1754
44	1833116CB1	1754		1785591H1 (BRAINOT10)	1	284
44	1833116CB1	1754		5172858H1 (EPITXTUT01)	331	588
44	1833116CB1	1754		1920612R6 (BRSTTUT01)	866	1402
45	001799CB1	2713	1-27, 1464-2008	5994129H1 (FTUBTUT02)	587	912
45	001799CB1	2713		4245126H1 (BRABDIT01)	1982	2239
45	001799CB1	2713		6818763J1 (BRAUNOR01)	1	549
45	001799CB1	2713		5054327H1 (COLATWT01)	1456	1726
45	001799CB1	2713		6739739H1 (BRAFDIT02)	2153	2713
45	001799CB1	2713		71336820V1	276	898
45	001799CB1	2713		3730557H1 (SMCCNON03)	884	1198
45	001799CB1	2713		644891R6 (BRSTTUT02)	1575	1981
45	001799CB1	2713		3515211H1 (LUNGNOT33)	1940	2217
45	001799CB1	2713		2691467T6 (LUNGNOT23)	907	1471
45	001799CB1	2713		3240741H1 (COLAUCT01)	1401	1685
45	001799CB1	2713		4771110H1 (BRATNOT02)	1715	1990
46	119814CB1	1768	1-688	2637776F6 (BONTNOT01)	968	1494
46	119814CB1	1768		119814R1 (MUSCNOT01)	739	1406
46	119814CB1	1768		2638913F6 (BONTNOT01)	1410	1768
46	119814CB1	1768		1993563H1 (CORENOT02)	656	940
46	119814CB1	1768		g2184959	349	846
46	119814CB1	1768		g1218792	1	579
46	119814CB1	1768		2395927T6 (THP1AZT01)	20	182

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
47	1295420CB1	3287	914-1321, 177-207	148434H1 (FIBRNGT01)	812	1028
47	1295420CB1	3287		2697808H1 (UTRSNOT12)	675	877
47	1295420CB1	3287		5778293H1 (BRAXNOT03)	1185	1447
47	1295420CB1	3287		2149151F6 (BRAINOT09)	1661	2176
47	1295420CB1	3287		2883729F6 (SINJNOT02)	1	515
47	1295420CB1	3287		1888639H1 (BLADTUT07)	868	1147
47	1295420CB1	3287		2154634F6 (BRAINOT09)	2720	3278
47	1295420CB1	3287		3703932T6 (PENCNOT07)	1334	2009
47	1295420CB1	3287		998245R1 (KIDNTUT01)	2118	2637
47	1295420CB1	3287		2223877F6 (SEMNOT01)	323	816
47	1295420CB1	3287		4027885H1 (BRAINOT23)	999	1261
47	1295420CB1	3287		835343R1 (PROSNOT07)	2247	2814
47	1295420CB1	3287		1367731R1 (SCORNON02)	2856	3287
48	1309364CB1	1748	1-49, 1037-1135	4701455H1 (SMCRTXT01)	1162	1416
48	1309364CB1	1748		4904644F6 (TYMNOT08)	799	1399
48	1309364CB1	1748		2914466F6 (THYMFET03)	1	536
48	1309364CB1	1748		5590953H1 (ENDINOT02)	678	933
48	1309364CB1	1748		1309364F6 (COLNFET02)	1227	1748
48	1309364CB1	1748		3727909H1 (SMCCNON03)	513	816
49	1315267CB1	2163	705-799	898915H1 (BRSTTUT03)	1839	2163
49	1315267CB1	2163		465550R6 (LATRNOT01)	673	1257
49	1315267CB1	2163		1575785F6 (LNODNOT03)	1029	1630
49	1315267CB1	2163		5191222F6 (OVARDIT06)	1	538
49	1315267CB1	2163		5207783F6 (BRAFNOT02)	426	1041
49	1315267CB1	2163		1315267F6 (BLADTUT02)	1434	2022
50	1403289CB1	1615	1119-1170	2811792T6 (OVARNOT10)	489	1121
50	1403289CB1	1615		059048R6 (MUSCNOT01)	1080	1615
50	1403289CB1	1615		3502723H1 (ADRENOT11)	932	1225
50	1403289CB1	1615		1403289F6 (LATRTUT02)	1	601
51	1607607CB1	1356	1-157, 1263-1356	7262994H1 (UTRETC01)	252	929
51	1607607CB1	1356		3467640F6 (BRAIDIT01)	350	1048
51	1607607CB1	1356		2137437H1 (ENDCNOT01)	1	275
51	1607607CB1	1356		1607607F6 (LUNGNOT15)	872	1356
52	1660025CB1	1268	1-88, 424- 459, 775-836	2580277F6 (KIDNTUT13)	213	932

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
52	1660025CB1	1268		2172241H1 (ENDCNOT03)	1	240
52	1660025CB1	1268		1988094R6 (LUNGAST01)	750	1268
52	1660025CB1	1268		1756804R6 (PITUNOT03)	248	966
53	1796836CB1	2554	1177-1245, 1-61	2280307T6 (PROSNON01)	687	1302
53	1796836CB1	2554		4971676H1 (HELATXT02)	1	227
53	1796836CB1	2554		2582430T6 (KIDNTUT13)	1198	1545
53	1796836CB1	2554		2497103T6 (ADRETUT05)	1949	2533
53	1796836CB1	2554		2534742H1 (BRAINOT18)	1527	1758
53	1796836CB1	2554		2553754T6 (THYMNOT03)	1817	2528
53	1796836CB1	2554		2726708H1 (OVARUT05)	1630	1863
53	1796836CB1	2554		276683H1 (TESTNOT03)	1311	1568
53	1796836CB1	2554		2938533H1 (THYMFET02)	1056	1326
53	1796836CB1	2554		6914750J1 (PITUDIR01)	47	684
53	1796836CB1	2554		2300549R6 (BRSTNOT05)	2162	2554
53	1796836CB1	2554		3030841F6 (HEARFET02)	319	877
54	2880670CB1	1216	605-636	2889280T7 (LUNGFET04)	489	1192
54	2880670CB1	1216		1358092F1 (LUNGNOT09)	246	920
54	2880670CB1	1216		816703R1 (OVARUT01)	657	1216
54	2880670CB1	1216		2529604H1 (GBLANOT02)	1	357
55	2913976CB1	1457	1-446, 1406-1457	3736188F6 (SMCCNOS01)	1173	1428
55	2913976CB1	1457		2913976F6 (KIDNTUT15)	1	520
55	2913976CB1	1457		4645636H1 (PROSTUT20)	1187	1449
55	2913976CB1	1457		4331439H1 (KIDNNOT32)	461	712
55	2913976CB1	1457		4643722H1 (PROSTWT03)	1108	1325
55	2913976CB1	1457		1312116F1 (COLNFET02)	583	1127
56	3092084CB1	1636	857-1636	1709866F6 (PROSNOT16)	1097	1634
56	3092084CB1	1636		2807436F6 (BLADTUT08)	1277	1636
56	3092084CB1	1636		6906626H1 (MUSLTDR02)	1	610
56	3092084CB1	1636		SBMA03169F1	597	1181
56	3092084CB1	1636		3092084F6 (BRSTNOT19)	543	1147
57	3882482CB1	1742	1-82, 923-994	2286328X19F1 (BRAINON01)	742	1251
57	3882482CB1	1742		2804312F6 (PENCNOT01)	299	926
57	3882482CB1	1742		986917T6 (LVENNOT03)	1088	1742
57	3882482CB1	1742		3175528F6 (UTRSTUT04)	1	317
57	3882482CB1	1742		1232503F6 (LUNGFET03)	960	1553

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
57	3882482CB1	1742		2286328X16F1 (BRAINON01)	402	969
58	4933451CB1	502	1-401	4931591H1 (BRSTTUT20)	341	602
58	4933451CB1	502		2502933F6 (CONUTUT01)	1	479
59	5043904CB1	3237	1964-2007, 2911-2969, 993-1057, 1328-1589	2153280F6 (BRAINOT09)	335	888
59	5043904CB1	3237		5043904R6 (PLACFER01)	1	583
59	5043904CB1	3237		075538H1 (THP1PEB01)	1604	1818
59	5043904CB1	3237		3189755X301D1 (THYMNON04)	1131	1674
59	5043904CB1	3237		2460935F6 (THYRN0T08)	614	1177
59	5043904CB1	3237		1795345R6 (PROSTUT05)	2026	2510
59	5043904CB1	3237		1865353F6 (PROSN0T19)	2686	3237
59	5043904CB1	3237		1365052R6 (SCORN0N02)	2440	2957
59	5043904CB1	3237		3250182H1 (SEMVN0T03)	1831	2128
59	5043904CB1	3237		4713986H1 (BRAIHCT01)	2266	2513
59	5043904CB1	3237		3804331H1 (BLADTUT03)	1777	2089
60	5202390CB1	3640	1412-1489, 2294-2508, 1-161, 3244-3640	2544502H2 (UTRSNOT11)	2656	2927
60	5202390CB1	3640		2321656R6 (OVARNOT02)	2039	2448
60	5202390CB1	3640		2557486F6 (THYMN0T03)	1	659
60	5202390CB1	3640		1441193F6 (THYRN0T03)	3317	3640
60	5202390CB1	3640		2844888H1 (DRGLN0T01)	864	1009
60	5202390CB1	3640		3705507H1 (PENCN0T07)	3047	3352
60	5202390CB1	3640		2122377F6 (BRSTN0T07)	2844	3297
60	5202390CB1	3640		4313841F6 (BRAFN0T01)	2322	2662
60	5202390CB1	3640		5092148H1 (UTRSTMR01)	685	961
60	5202390CB1	3640		94240294_CD	525	3562
60	5202390CB1	3640		1944075H1 (PITUN0T01)	1590	1851
60	5202390CB1	3640		3493516H1 (ADRETUT07)	1999	2279
60	5202390CB1	3640		176099H1 (TYLNM0T01)	411	738
60	5202390CB1	3640		2851783H1 (BRSTTUT13)	2600	2796
60	5202390CB1	3640		534176R1 (BRAINOT03)	1041	1567
60	5202390CB1	3640		4107451H1 (BRSTTUT17)	1431	1694
60	5202390CB1	3640		2842892F6 (DRGLN0T01)	1604	2220

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
61	5526375CB1	2111	1-50, 1540-2111	3038423H1 (BRSTNOT16)	1004	1278
61	5526375CB1	2111		2513433F6 (LIVRTUT04)	1600	2111
61	5526375CB1	2111		3534575H1 (KIDNNOT25)	1263	1529
61	5526375CB1	2111		2993194F6 (KIDNFET02)	729	1224
61	5526375CB1	2111		5109694H1 (PROSTUS19)	1385	1626
61	5526375CB1	2111		2993263H1 (KIDNFET02)	1242	1479
61	5526375CB1	2111		3534157H1 (KIDNNOT25)	518	788
61	5526375CB1	2111		2580307F6 (KIDNTUT13)	1	519
61	5526375CB1	2111		2070882F6 (ISLATNOT01)	225	715
62	5677408CB1	1389	1-177	535789R1 (ADRENOT03)	1079	1389
62	5677408CB1	1389		881149T6 (THYRNOT02)	793	1378
62	5677408CB1	1389		6023544H1 (TESTNOT11)	736	1017
62	5677408CB1	1389		881149R6 (THYRNOT02)	1	772
63	5982278CB1	3331	809-1149, 1755-1989	5260541H1 (CONDUTUT01)	2203	2470
63	5982278CB1	3331		1390622H1 (EOSINOT01)	2029	2257
63	5982278CB1	3331		4515063H1 (EPIMNOT01)	1740	1993
63	5982278CB1	3331		3584113H1 (293TF4T01)	2462	2796
63	5982278CB1	3331		3405843H1 (ESOGNOT03)	919	1174
63	5982278CB1	3331		5261482H1 (CONDUTUT01)	2611	2862
63	5982278CB1	3331		1637273H1 (UTRSNOT06)	1619	1733
63	5982278CB1	3331		g1521431	2559	3331
63	5982278CB1	3331		3591491H1 (293TF5T01)	1674	1981
63	5982278CB1	3331		4957640H1 (TLYMNOT05)	1464	1726
63	5982278CB1	3331		4666088H1 (MEGBUNT01)	2280	2536
63	5982278CB1	3331		043258H1 (TBLYNOT01)	1370	1562
63	5982278CB1	3331		2907496F6 (THYMNOT05)	24	624
63	5982278CB1	3331		4983673H1 (HELATXT05)	1865	2134
63	5982278CB1	3331		g34671_CD	130	3166
63	5982278CB1	3331		3449505X304D1 (UTRSNON03)	942	1450
63	5982278CB1	3331		2640427T6 (LUNGTFUT08)	2646	3309
63	5982278CB1	3331		2205131F6 (SPLNFET02)	1	514
64	6437362CB1	3558	1-428, 3352-3558, 923-1583	720069R6 (SYNOOAT01)	3159	3558
64	6437362CB1	3558		2785980H1 (BRSTNOT13)	2462	2730
64	6437362CB1	3558		1568793H1 (UTRSNOT05)	1264	1467

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
64	6437362CB1	3558		987366H1 (LVENNOT03)	763	1088
64	6437362CB1	3558		95689540_CD	678	3298
64	6437362CB1	3558		4567664F6 (HELATXT01)	1	500
64	6437362CB1	3558		1988667R6 (LJNGAST01)	2160	2709
64	6437362CB1	3558		4980789H1 (HELATXT04)	981	1248
64	6437362CB1	3558		6437362H1 (LJNGNON07)	432	1052
64	6437362CB1	3558		2903936F6 (DRGCNOT01)	1760	2328
64	6437362CB1	3558		3208061H1 (PENCNOT03)	2706	2948
64	6437362CB1	3558		3288660F6 (BONRFET01)	1433	2050
64	6437362CB1	3558		865171R1 (BRAITUT03)	2929	3483
65	4173970CB1	5373	3418-5373, 1-186, 1641-2444, 857-1058	829704R1 (PROSTUT04)	1356	1950
65	4173970CB1	5373		5604442H1 (MONOTXN03)	2038	2310
65	4173970CB1	5373		1708630F6 (PROSNOT16)	3923	4539
65	4173970CB1	5373		4561514F6 (KERATXT01)	4397	5197
65	4173970CB1	5373		1437088F1 (PANCNOT08)	3691	4247
65	4173970CB1	5373		1433309R1 (BEPINON01)	3666	4214
65	4173970CB1	5373		4167822F6 (PANCNOT21)	1	494
65	4173970CB1	5373		1806736F6 (SINTNOT13)	5043	5373
65	4173970CB1	5373		3508537F6 (CONCNOT01)	2520	3017
65	4173970CB1	5373		4173970F6 (SINTNOT21)	2115	2677
65	4173970CB1	5373		2277402R6 (PROSNON01)	660	1229
65	4173970CB1	5373		1708630T6 (PROSNOT16)	4639	5347
65	4173970CB1	5373		5944958H1 (COLADIT05)	1710	2018
65	4173970CB1	5373		1300156F1 (BRSTNOT07)	1133	1687
65	4173970CB1	5373		92737563	1885	2171
65	4173970CB1	5373		209752R1 (SPLNNOT02)	3040	3690
65	4173970CB1	5373		287603R1 (EOSIHT02)	210	966
65	4173970CB1	5373		3091106H1 (BRSTNOT19)	4284	4560
65	4173970CB1	5373		516280R6 (MMLR1DT01)	2996	3438
66	2772751CB1	4333	2456-3205, 100-160, 1-23, 1459-1957, 3695-4333	70475866V1	507	1008
66	2772751CB1	4333		70472414V1	2045	2690

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
66	2772751CB1	4333		3402774HL (ESOGNOT03)	1	256
66	2772751CB1	4333		70475304V1	1481	2093
66	2772751CB1	4333		70475403V1	976	1554
66	2772751CB1	4333		70470913V1	1545	2109
66	2772751CB1	4333		70747026V1	3561	4054
66	2772751CB1	4333		g3923880	319	678
66	2772751CB1	4333		1298255T6 (BRSTNOT07)	3001	3690
66	2772751CB1	4333		70472159V1	1049	1556
66	2772751CB1	4333		70472656V1	2219	2925
66	2772751CB1	4333		g5340324	24	467
66	2772751CB1	4333		6849173HL (KIDNTMN03)	3801	4333
66	2772751CB1	4333		6221536U1	2737	3452
67	2793768CB1	2213	2186-2213, 1066-1156	70843048V1	1646	2213
67	2793768CB1	2213		2026465R6 (KERANOT02)	709	1268
67	2793768CB1	2213		7712268HL (TESTTUE02)	1621	2213
67	2793768CB1	2213		g1958420	1	421
67	2793768CB1	2213		6584157HL (ESOGTMC01)	984	1576
67	2793768CB1	2213		2793768F6 (COLNTUT16)	131	777
67	2793768CB1	2213		71279716V1	1510	2183
68	3035248CB1	1142	1-55, 555-605	71515027V1	585	1140
68	3035248CB1	1142		71486327V1	402	787
68	3035248CB1	1142		71514455V1	1	576

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
35	1889577CB1	PROSTUT12
36	2427982CB1	DRGCNOT01
37	2470833CB1	LUNGAST01
38	2080579CB1	UTRSNOT08
39	2156553CB1	THYMFET03
40	2182855CB1	SCORNOT04
41	2242106CB1	COLNPOT01
42	2726877CB1	LUNGNOT34
43	2738233CB1	MENITUT03
44	1833116CB1	THYRNOT03
45	001799CB1	BRSTTUT02
46	119814CB1	MUSCNOT01
47	1295420CB1	BRAITUT12
48	1309364CB1	TYLMUNT01
49	1315267CB1	BLADTUT02
50	1403289CB1	LATRTUT02
51	1607607CB1	BRAIDIT01
52	1660025CB1	BRAWNOT01
53	1796836CB1	BRSTNOT05
54	2880670CB1	OVARTUT01
55	2913976CB1	ENDCNOT04
56	3092084CB1	HEAANOT01
57	3882482CB1	SPLNNOT11
58	4933451CB1	BRSTTUT20
59	5043904CB1	PLACFER01
60	5202390CB1	TESTTUT02
61	5526375CB1	KIDNFET02
62	5677408CB1	ADRENOT03
63	5982278CB1	SPLNFET02
64	6437362CB1	BRAINOT23
65	4173970CB1	BRSTNOT07
66	2772751CB1	BRSTNOT07
67	2793768CB1	UTRSNOT12
68	3035248CB1	TYLMNOT05

Table 6

Library	Vector	Library Description
ADRENOT03	PSPORT1	Library was constructed using RNA isolated from the adrenal tissue of a 17-year-old Caucasian male, who died from cerebral anoxia.
BLADTUT02	pINCY	Library was constructed using RNA isolated from bladder tumor tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology indicated grade 3 invasive transitional cell carcinoma. Family history included acute renal failure, osteoarthritis, and atherosclerosis.
BRAIDIT01	pINCY	Library was constructed using RNA isolated from diseased brain tissue. Patient history included multiple sclerosis, type II lesion.
BRAINOT23	pINCY	Library was constructed using RNA isolated from right temporal lobe tissue removed from a 45-year-old Black male during a brain lobectomy. Pathology for the associated tumor tissue indicated dysembryoplastic neuroepithelial tumor of the right temporal lobe. The right temporal region dura was consistent with calcifying pseudotumor of the neuraxis. The patient presented with convulsive intractable epilepsy, partial epilepsy, and memory disturbance. Patient history included obesity, meningitis, backache, unspecified sleep apnea, acute stressreaction, acquired knee deformity, and chronic sinusitis. Family history included obesity, benign hypertension, cirrhosis of the liver, alcohol abuse, hyperlipidemia, cerebrovascular disease, and type II diabetes.
BRAITUT12	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 40-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated grade 4 gemistocytic astrocytoma.
BRAWNOT01	pINCY	Library was constructed using RNA isolated from dentate nucleus tissue removed from the brain of a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomeningeal fibrosis and multiple microinfarctions of the cerebral neocortex. Grossly, the brain regions examined and cranial nerves were unremarkable, showing no evidence of atrophy. No atherosclerosis of the major vessels was noted. Microscopically, the cerebral hemisphere revealed moderate fibrosis of the leptomeninges with focal calcifications. There was evidence of shrunken and slightly eosinophilic pyramidal neurons throughout the cerebral hemispheres. There were also multiple small microscopic areas of cavitation with surrounding gliosis scattered throughout the cerebral cortex. Special stains with Bielschowsky silver, Klüver-Barrera, and Congo Red revealed no evidence of neurofibrillary tangles or diffuse anorectic amyloid plaques, demyelination, and cerebral amyloid angiopathy, respectively. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly, and an enlarged spleen and liver. Patient medications included simethicone, lasix, Digoxin, Colace, Zantac, captopril, and Vasotec.
BRSTNOT05	PSPORT1	Library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.

Table 6 (cont.)

Library	Vector	Library Description
BRSTNOT07	pINCY	Library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.
BRSTNOT07	pINCY	Library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.
BRSTTUT02	PSPORT1	Library was constructed using RNA isolated from breast tumor tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy with reconstruction. Pathology indicated residual invasive grade 3 mammary ductal adenocarcinoma. The remaining breast parenchyma exhibited proliferative fibrocystic changes without atypia. One of 10 axillary lymph nodes had metastatic tumor as a microscopic intranodal focus. Patient history included kidney infection and condyloma acuminatum. Family history included benign hypertension, hyperlipidemia, and a malignant colon neoplasm.
BRSTTUT20	pINCY	Library was constructed using RNA isolated from left breast tumor tissue removed from a 66-year-old Black female during a unilateral extended simple mastectomy and fine needle breast biopsy. Pathology indicated invasive grade 4, nuclear grade 3 adenocarcinoma ductal type, diffusely replacing the left breast. The skin, nipple and fascia were all involved, including the deep surgical margin. Extensive angiolymphatic invasion was identified, including superficial dermal lymphatics. Metastatic grade 4 adenocarcinoma completely replaced 6 lymph nodes with extranodal extension. Multiple low axillary lymph nodes tissue were positive for metastatic mammary carcinoma. Left chest wall biopsy indicated metastatic grade 4 adenocarcinoma. Prior left breast biopsy indicated metastatic grade 4, nuclear grade 3, metastatic mammary carcinoma. The patient presented with malaise and fatigue. Patient history included secondary malignant neoplasm of the liver, secondary malignant neoplasm of the brain/spine, deficiency anemia, type II diabetes, chronic renal failure, and normal delivery. Patient medications included two cycles of cyclophosphamide/epirubicin and 5-Fluorouracil in November 1995. Family history included benign hypertension, type II diabetes, hyperlipidemia, and depressive disorder in the mother.
COLNPOT01	pINCY	Library was constructed using RNA isolated from colon polyp tissue removed from a 40-year-old Caucasian female during a total colectomy. Pathology indicated an inflammatory pseudopolyp; this tissue was associated with a focally invasive grade 2 adenocarcinoma and multiple tubovillous adenomas. Patient history included a benign neoplasm of the bowel.

Table 6 (cont.)

Library	Vector	Library Description
DRGCNOT01	pINCY	Library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
ENDCNOT04	pINCY	Library was constructed using RNA isolated from coronary artery endothelial cell tissue removed from a 3-year-old Caucasian male.
HEAANOT01	pINCY	Library was constructed using RNA isolated from right coronary and right circumflex coronary artery tissue removed from the explanted heart of a 46-year-old Caucasian male during a heart transplantation. Patient history included myocardial infarction from total occlusion of the left anterior descending coronary artery, atherosclerotic coronary artery disease, hyperlipidemia, myocardial ischemia, dilated cardiomyopathy, left ventricular dysfunction, and tobacco abuse. Previous surgeries included cardiac catheterization. Family history included atherosclerotic coronary artery disease.
KIDNFET02	pINCY	Library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart and died at 23 weeks' gestation.
LATRTUT02	pINCY	Library was constructed using RNA isolated from a myxoma removed from the left atrium of a 43-year-old Caucasian male during annuloplasty. Pathology indicated atrial myxoma. Patient history included pulmonary insufficiency, acute myocardial infarction, atherosclerotic coronary artery disease, hyperlipidemia, and tobacco use. Family history included benign hypertension, acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
LUNGAST01	PSPORT1	Library was constructed using RNA isolated from the lung tissue of a 17-year-old Caucasian male, who died from head trauma. Patient history included asthma.
LUNGNOT34	pINCY	Library was constructed using RNA isolated from lung tissue removed from a 12-year-old Caucasian male.
MENITUT03	pINCY	Library was constructed using RNA isolated from brain meningioma tissue removed from a 35-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a benign neoplasm in the right cerebellopontine angle of the brain. Patient history included hypothyroidism. Family history included myocardial infarction and breast cancer.
MUSCNOT01	PBLUESCRIPT	Library was constructed at Stratagene (SFE937209), using RNA isolated from the skeletal muscle tissue of a patient with malignant hyperthermia.

Table 6 (cont.)

Library	Vector	Library Description
OVARTUT01	PSPORT1	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
PLACFER01	pINCY	The library was constructed using RNA isolated from placental tissue removed from a Caucasian fetus, who died after 16 weeks' gestation from fetal demise and hydrocephalus. Patient history included umbilical cord wrapped around the head (3 times) and the shoulders (1 time). Serology was positive for anti-CMV. Family history included multiple pregnancies and live births, and an abortion.
PROSTUT12	pINCY	Library was constructed using RNA isolated from prostate tumor tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated an adenocarcinoma (Gleason grade 2+2). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA).
SCORNOT04	pINCY	Library was constructed using RNA isolated from cervical spinal cord tissue removed from a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
SPLNFET02	pINCY	Library was constructed using RNA isolated from spleen tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation.
SPLNNOT11	pINCY	Library was constructed using RNA isolated from diseased spleen tissue removed from a 14-year-old Asian male during a total splenectomy. Pathology indicated changes consistent with idiopathic thrombocytopenic purpura. The patient presented with bruising. Patient medications included Vincristine.
TESTTUT02	pINCY	Library was constructed using RNA isolated from testicular tumor removed from a 31-year-old Caucasian male during unilateral orchiectomy. Pathology indicated embryonal carcinoma.
THYMFET03	pINCY	Library was constructed using RNA isolated from thymus tissue removed from a Caucasian male fetus.
THYRNOT03	pINCY	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma, forming a well-encapsulated mass in the left thyroid.
TYMNOT05	pINCY	Library was constructed RNA isolated from nonactivated Th2 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-4 in the presence of anti-IL-12 antibodies and B7-transfected COS cells.

Table 6 (cont.)

Library	Vector	Library Description
TYMUNT01	pINCY	Library was constructed using RNA isolated from resting allogenic T-lymphocyte tissue removed from an adult (40-50-year-old) Caucasian male.
UTRSNOT08	pINCY	Library was constructed using RNA isolated from uterine tissue removed from a 35-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated that the endometrium was secretory phase with a benign endometrial polyp 1 cm in diameter. The cervix showed mild chronic cervicitis. Family history included atherosclerotic coronary artery disease and type II diabetes.
UTRSNOT12	pINCY	Library was constructed using RNA isolated from uterine myometrial tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Pathology for the associated tumor tissue indicated uterine leiomyoma. Patient history included ventral hernia and a benign ovarian neoplasm.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1998) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-34,
 - b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-34,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, and
10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34.
2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-34.
15
3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
- 20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:35-68.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
25
7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
- 30 9. A method for producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
35 b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.
11. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting
 - 5 of SEQ ID NO:35-68,
 - b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:35-68,
 - c) a polynucleotide complementary to a polynucleotide of a),
 - d) a polynucleotide complementary to a polynucleotide of b), and
 - 10 e) an RNA equivalent of a)-d).
12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.
13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization
 - 20 complex is formed between said probe and said target polynucleotide or fragments thereof, and
 - b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.
14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.
15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
 - 30 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

35

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-34.

18. A method for treating a disease or condition associated with decreased expression of functional CYSKP, comprising administering to a patient in need of such treatment the composition of claim 16.

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional CYSKP, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional CYSKP, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a

compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

- 5 a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in
- 10 the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method

15 comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of
- 20 the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at
- 25 least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- 30 d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of CYSKP in a biological sample comprising the steps of:

- a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
- 5 b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

30. The antibody of claim 10, wherein the antibody is:

- a) a chimeric antibody,
- 10 b) a single chain antibody,
- c) a Fab fragment,
- d) a F(ab')₂ fragment, or
- e) a humanized antibody.

15 31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of CYSKP in a subject, comprising administering to said subject an effective amount of the composition of claim 31.

20

33. A composition of claim 31, wherein the antibody is labeled.

34. A method of diagnosing a condition or disease associated with the expression of CYSKP in a subject, comprising administering to said subject an effective amount of the composition of claim 33.

25

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
- 30 b) isolating antibodies from said animal; and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the

group consisting of SEQ ID NO:1-34.

36. An antibody produced by a method of claim 35.

5 37. A composition comprising the antibody of claim 36 and a suitable carrier.

38. A method of making a monoclonal antibody with the specificity of the antibody of claim
10 comprising:

- 10 a) immunizing an animal with a polypeptide having an amino acid sequence selected from
the group consisting of SEQ ID NO:1-34, or an immunogenic fragment thereof, under conditions to
elicit an antibody response;
- b) isolating antibody producing cells from the animal;
- c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-
producing hybridoma cells;
- 15 d) culturing the hybridoma cells; and
- e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide
having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34.

39. A monoclonal antibody produced by a method of claim 38.

20

40. A composition comprising the antibody of claim 39 and a suitable carrier.

41. The antibody of claim 10, wherein the antibody is produced by screening a Fab
expression library.

25

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant
immunoglobulin library.

43. A method for detecting a polypeptide having an amino acid sequence selected from the
30 group consisting of SEQ ID NO:1-34 in a sample, comprising the steps of:

- a) incubating the antibody of claim 10 with a sample under conditions to allow specific
binding of the antibody and the polypeptide; and
- b) detecting specific binding, wherein specific binding indicates the presence of a
polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34 in

the sample.

44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34 from a sample, the method comprising:

- 5 a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and
- b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-34.

10 45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

15

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

20

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

25

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

30

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

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60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
- 10
62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.
64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.
- 15
65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.
66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.
- 20
67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.
68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.
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- 25
70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.
71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:27.
- 30
72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.
73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.
74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.

75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:31.
76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:32.
- 5 77. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:33.
78. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:34.
- 10 79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:35.
80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.
- 15 81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.
82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.
- 20 83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.
84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.
- 25 85. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:41.
- 30 86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:42.
87. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:43.

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- 5 100. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:56.
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- 10 102. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:58.
103. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:59.
- 15 104. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:60.
- 20 105. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:61.
106. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:62.
- 25 107. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:63.
108. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:64.
- 30 109. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:65.

110. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:66.

111. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
5 NO:67.

112. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:68.

<110> INCYTE GENOMICS, INC.
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 LU, Dyung Aina M.
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 LAL, Preeti
 YAO, Monique G.
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Thr Gln Pro Phe Ser Leu Lys Asn Leu Asp Asn Ser Val His Leu
155     160     165
Cys Asn Asn Ser Ile Gln Lys His Leu Glu Asn Ser Cys His Arg
170     175     180
His Pro Leu Leu Pro Pro Asp Asn Met Trp Ser Ser Gln Arg Phe
185     190     195
Gln Ala His Leu Gln Glu Met Gly Ala Pro Asn Ala Trp Ser Thr
200     205     210
Ile Ile Val Pro Gly Met Lys Asp Ala Val Ile His Ala Leu Gln
215     220     225
Thr Ser Gln Asp Thr Val Gln Cys Arg Lys Ala Ser Phe Glu Leu
230     235     240
Tyr Gly Ala Asp Phe Val Phe Gly Glu Asp Phe Gln Pro Trp Leu
245     250     255
Ile Glu Ile Asn Ala Ser Pro Thr Met Ala Pro Ser Thr Ala Val
260     265     270
Thr Ala Arg Leu Cys Ala Gly Val Gln Ala Asp Thr Leu Arg Val
275     280     285
Val Ile Asp Arg Met Leu Asp Arg Asn Cys Asp Thr Gly Ala Phe
290     295     300
Glu Leu Ile Tyr Lys Gln Pro Ala Val Glu Val Pro Gln Tyr Val
305     310     315
Gly Ile Arg Leu Leu Val Glu Gly Phe Thr Ile Lys Lys Pro Met
320     325     330
Ala Met Cys His Arg Arg Met Gly Val Arg Pro Ala Val Pro Leu
335     340     345
Leu Thr Gln Arg Gly Ser Gly Glu Gly Lys Asp Ser Gly Ile Pro
350     355     360
Thr His Arg Ser Ala Ser Arg Lys Gly Thr Gly Ala Arg Ser Leu
365     370     375
Gly His Ser Glu Lys Pro Val Ser Thr Ala Thr Thr Ser Ala Pro
380     385     390
Gly Lys Gly Lys Lys Gly Lys Ala Lys Arg Ala Thr Ala Leu Val
395     400     405
Cys Pro Asn Leu Trp Glu Trp Asp Ala Pro Ser Thr Arg Met Gly
410     415     420
Cys Ile Phe Thr Met Thr Phe Ser Ser Gly Asp Arg Gln Pro His
425     430     435
His Leu Asn Arg Leu Pro Leu Ser Pro Lys Asn Pro Gln Ala Leu
440     445     450
Gly Lys Thr Ile Pro Pro Lys His Pro Ser Val Pro Arg Arg Phe
455     460     465
Ile Pro Ala Leu Gln Ala Pro Pro Asn His Leu Asp Gln Pro Pro

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470
 His Gln Arg Ala Thr Ser Ser Lys
 485

475
 480

<210> 6
 <211> 1190
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 2182855CD1

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 1 5 10 15
 Glu Leu Asn Ala Asn Leu Ser Asn Leu Thr Ser Ala Phe Glu Lys
 20 25 30
 Ala Thr Ala Glu Lys Ile Lys Cys Gln Glu Ala Asp Ala Thr
 35 40 45
 Asn Arg Val Ile Leu Leu Ala Asn Arg Leu Val Gly Gly Leu Ala
 50 55 60
 Ser Glu Asn Ile Arg Trp Ala Glu Ser Val Glu Asn Phe Arg Ser
 65 70 75
 Gln Gly Val Thr Leu Cys Gly Asp Val Leu Leu Ile Ser Ala Phe
 80 85 90
 Val Ser Tyr Val Gly Tyr Phe Thr Lys Lys Tyr Arg Asn Glu Leu
 95 100 105
 Met Glu Lys Phe Trp Ile Pro Tyr Ile His Asn Leu Lys Val Pro
 110 115 120
 Ile Pro Ile Thr Asn Gly Leu Asp Pro Leu Ser Leu Leu Thr Asp
 125 130 135
 Asp Ala Asp Val Ala Thr Trp Asn Asn Gln Gly Leu Pro Ser Asp
 140 145 150
 Arg Met Ser Thr Glu Asn Ala Thr Ile Leu Gly Asn Thr Glu Arg
 155 160 165
 Trp Pro Leu Ile Val Asp Ala Gln Leu Gln Gly Ile Lys Trp Ile
 170 175 180
 Lys Asn Lys Tyr Arg Ser Glu Leu Lys Ala Ile Arg Leu Gly Gln
 185 190 195
 Lys Ser Tyr Leu Asp Val Ile Glu Gln Ala Ile Ser Glu Gly Asp
 200 205 210
 Thr Leu Leu Ile Glu Asn Ile Gly Glu Thr Val Asp Pro Val Leu
 215 220 225
 Asp Pro Leu Leu Gly Arg Asn Thr Ile Lys Lys Gly Lys Tyr Ile
 230 235 240
 Lys Ile Gly Asp Lys Glu Val Glu Tyr His Pro Lys Phe Arg Leu
 245 250 255
 Ile Leu His Thr Lys Tyr Phe Asn Pro His Tyr Lys Pro Glu Met
 260 265 270
 Gln Ala Gln Cys Thr Leu Ile Asn Phe Leu Val Thr Arg Asp Gly
 275 280 285
 Leu Glu Asp Gln Leu Leu Ala Ala Val Val Ala Lys Glu Arg Pro
 290 295 300
 Asp Leu Glu Gln Leu Lys Ala Asn Leu Thr Lys Ser Gln Asn Glu
 305 310 315
 Phe Lys Ile Val Leu Lys Glu Leu Glu Asp Ser Leu Leu Ala Arg
 320 325 330
 Leu Ser Ala Ala Ser Gly Asn Phe Leu Gly Asp Thr Ala Leu Val
 335 340 345
 Glu Asn Leu Glu Thr Thr Lys His Thr Ala Ser Glu Ile Glu Glu
 350 355 360
 Lys Val Val Glu Ala Lys Ile Thr Glu Val Lys Ile Asn Glu Ala
 365 370 375
 Arg Glu Asn Tyr Arg Pro Ala Ala Glu Arg Ala Ser Leu Leu Tyr
 380 385 390
 Phe Ile Leu Asn Asp Leu Asn Lys Ile Asn Pro Val Tyr Gln Phe

	395		400		405
Ser Leu Lys Ala	Phe Asn Val Val Phe	Glu Lys Ala Ile Gln	Arg		
	410		415		420
Thr Thr Pro Ala	Asn Glu Val Lys Gln	Arg Val Ile Asn Leu	Thr		
	425		430		435
Asp Glu Ile Thr	Tyr Ser Val Tyr Met	Tyr Thr Ala Arg Gly	Leu		
	440		445		450
Phe Glu Arg Asp	Lys Leu Ile Phe Leu	Ala Gln Val Thr Phe	Gln		
	455		460		465
Val Leu Ser Met	Lys Lys Glu Leu Asn	Pro Val Glu Leu Asp	Phe		
	470		475		480
Leu Leu Arg Phe	Pro Phe Lys Ala Gly	Val Val Ser Pro Val	Asp		
	485		490		495
Phe Leu Gln His	Gln Gly Trp Gly Gly	Ile Lys Ala Leu Ser	Glu		
	500		505		510
Met Asp Glu Phe	Lys Asn Leu Asp Ser	Asp Ile Glu Gly Ser	Ala		
	515		520		525
Lys Arg Trp Lys	Lys Leu Val Glu Ser	Glu Ala Pro Glu Lys	Glu		
	530		535		540
Ile Phe Pro Lys	Glu Trp Lys Asn Lys	Thr Ala Leu Gln Lys	Leu		
	545		550		555
Cys Met Val Arg	Cys Leu Arg Pro Asp	Arg Met Thr Tyr Ala	Ile		
	560		565		570
Lys Asn Phe Val	Glu Glu Lys Met Gly	Ser Lys Phe Val Glu	Gly		
	575		580		585
Arg Ser Val Glu	Phe Ser Lys Ser Tyr	Glu Glu Ser Ser Pro	Ser		
	590		595		600
Thr Ser Ile Phe	Phe Ile Leu Ser Pro	Gly Val Asp Pro Leu	Lys		
	605		610		615
Asp Val Glu Ala	Leu Gly Lys Lys Leu	Gly Phe Thr Ile Asp	Asn		
	620		625		630
Gly Lys Leu His	Asn Val Ser Leu Gly	Gln Gly Gln Glu Val	Val		
	635		640		645
Ala Glu Asn Ala	Leu Asp Val Ala Ala	Glu Lys Gly His Trp	Val		
	650		655		660
Ile Leu Gln Asn	Ile His Leu Val Ala	Arg Trp Leu Gly Thr	Leu		
	665		670		675
Asp Lys Lys Leu	Glu Arg Tyr Ser Thr	Gly Ser His Glu Asp	Tyr		
	680		685		690
Arg Val Phe Ile	Ser Ala Glu Pro Ala	Pro Ser Pro Glu Thr	His		
	695		700		705
Ile Ile Pro Gln	Gly Ile Leu Glu Asn	Ala Ile Lys Ile Thr	Asn		
	710		715		720
Glu Pro Pro Thr	Gly Met Tyr Ala Asn	Leu His Lys Ala Leu	Asp		
	725		730		735
Leu Phe Thr Gln	Asp Thr Leu Glu Met	Cys Thr Lys Glu Met	Glu		
	740		745		750
Phe Lys Cys Met	Leu Phe Ala Leu Cys	Tyr Phe His Ala Val	Val		
	755		760		765
Ala Glu Arg Arg	Lys Phe Gly Ala Gln	Gly Trp Asn Arg Ser	Tyr		
	770		775		780
Pro Phe Asn Asn	Gly Asp Leu Thr Ile	Ser Ile Asn Val Leu	Tyr		
	785		790		795
Asn Tyr Leu Glu	Ala Asn Pro Lys Val	Pro Trp Asp Asp Leu	Arg		
	800		805		810
Tyr Leu Phe Gly	Glu Ile Met Tyr Gly	Gly His Ile Thr Asp	Asp		
	815		820		825
Trp Asp Arg Arg	Leu Cys Arg Thr Tyr	Leu Ala Glu Tyr Ile	Arg		
	830		835		840
Thr Glu Met Leu	Glu Gly Asp Val Leu	Leu Ala Pro Gly Phe	Gln		
	845		850		855
Ile Pro Pro Asn	Leu Asp Tyr Lys Gly	Tyr His Glu Tyr Ile	Asp		
	860		865		870
Glu Asn Leu Pro	Pro Glu Ser Pro Tyr	Leu Tyr Gly Leu His	Pro		
	875		880		885
Asn Ala Glu Ile	Gly Phe Leu Thr Val	Thr Ser Glu Lys Leu	Phe		
	890		895		900


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Arg Thr Val Leu Glu Met Gln Pro Lys Glu Thr Asp Ser Gly Ala
      905      910      915
Gly Thr Gly Val Ser Arg Glu Glu Lys Val Lys Ala Val Leu Asp
      920      925      930
Asp Ile Leu Glu Lys Ile Pro Glu Thr Phe Asn Met Ala Glu Ile
      935      940      945
Met Ala Lys Ala Ala Glu Lys Thr Pro Tyr Val Val Val Ala Phe
      950      955      960
Gln Glu Cys Glu Arg Met Asn Ile Leu Thr Asn Glu Met Arg Arg
      965      970      975
Ser Leu Lys Glu Leu Asn Leu Gly Leu Lys Gly Glu Leu Thr Ile
      980      985      990
Thr Thr Asp Val Glu Asp Leu Ser Thr Ala Leu Phe Tyr Asp Thr
      995      1000      1005
Val Pro Asp Thr Trp Val Ala Arg Ala Tyr Pro Ser Met Met Gly
      1010      1015      1020
Leu Ala Ala Trp Tyr Ala Asp Leu Leu Leu Arg Ile Arg Glu Leu
      1025      1030      1035
Glu Ala Trp Thr Thr Asp Phe Ala Leu Pro Thr Thr Val Trp Leu
      1040      1045      1050
Ala Gly Phe Phe Asn Pro Gln Ser Phe Leu Thr Ala Ile Met Gln
      1055      1060      1065
Ser Met Ala Arg Lys Asn Glu Trp Pro Leu Asp Lys Met Cys Leu
      1070      1075      1080
Ser Val Glu Val Thr Lys Lys Asn Arg Glu Asp Met Thr Ala Pro
      1085      1090      1095
Pro Arg Glu Gly Ser Tyr Val Tyr Gly Leu Phe Met Glu Gly Ala
      1100      1105      1110
Arg Trp Asp Thr Gln Thr Gly Val Ile Ala Glu Ala Arg Leu Lys
      1115      1120      1125
Glu Leu Thr Pro Ala Met Pro Val Ile Phe Ile Lys Ala Ile Pro
      1130      1135      1140
Val Asp Arg Met Glu Thr Lys Asn Ile Tyr Glu Cys Pro Val Tyr
      1145      1150      1155
Lys Thr Arg Ile Arg Gly Pro Thr Tyr Val Trp Thr Phe Asn Leu
      1160      1165      1170
Lys Thr Lys Glu Lys Ala Ala Lys Trp Ile Leu Ala Ala Val Ala
      1175      1180      1185
Leu Leu Leu Gln Val
      1190

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<210> 7

<211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2242106CD1

<400> 7

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Met Leu Leu Thr Gln Val Val Trp Leu Pro Glu Pro Gly His Ser
  1      5      10      15
His Arg Phe Gln Val Leu Ser Val Ala Thr Asp Gly Lys Val Leu
  20      25      30
Leu Trp Gln Gly Ile Gly Val Gly Gln Leu Gln Leu Thr Glu Gly
  35      40      45
Phe Ala Leu Val Met Gln Gln Leu Pro Arg Ser Thr Lys Leu Lys
  50      55      60
Lys His Pro Arg Gly Glu Thr Glu Val Gly Ala Thr Ala Val Ala
  65      70      75
Phe Ser Ser Phe Asp Pro Arg Leu Phe Ile Leu Gly Thr Glu Gly
  80      85      90
Gly Phe Pro Leu Lys Cys Ser Leu Ala Ala Gly Glu Ala Ala Leu
  95      100      105
Thr Arg Met Pro Ser Ser Val Pro Leu Arg Ala Pro Ala Gln Phe
  110      115      120

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Thr	Phe	Ser	Pro	His	Gly	Gly	Pro	Ile	Tyr	Ser	Val	Ser	Cys	Ser
				125					130					135
Pro	Phe	His	Arg	Asn	Leu	Phe	Leu	Ser	Ala	Gly	Thr	Asp	Gly	His
				140					145					150
Val	His	Leu	Tyr	Ser	Met	Leu	Gln	Ala	Pro	Pro	Leu	Thr	Ser	Leu
				155					160					165
Gln	Leu	Ser	Leu	Lys	Tyr	Leu	Phe	Ala	Val	Arg	Trp	Ser	Pro	Val
				170					175					180
Arg	Pro	Leu	Val	Phe	Ala	Ala	Ala	Ser	Gly	Lys	Gly	Asp	Val	Gln
				185					190					195
Leu	Phe	Asp	Leu	Gln	Lys	Ser	Ser	Gln	Lys	Pro	Thr	Val	Leu	Ile
				200					205					210
Lys	Gln	Thr	Gln	Asp	Glu	Ser	Pro	Val	Tyr	Cys	Leu	Glu	Phe	Asn
				215					220					225
Ser	Gln	Gln	Thr	Gln	Leu	Leu	Ala	Ala	Gly	Asp	Ala	Gln	Gly	Thr
				230					235					240
Val	Lys	Val	Trp	Gln	Leu	Ser	Thr	Glu	Phe	Thr	Glu	Gln	Gly	Pro
				245					250					255
Arg	Glu	Ala	Glu	Asp	Leu	Asp	Cys	Leu	Ala	Ala	Glu	Val	Ala	Ala
				260					265					270

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<210> 8
<211> 647
<212> PRT
<213> Homo sapiens
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<221> misc_feature  
<223> Incyte ID No: 2726877CD1
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Met	Asp	Leu	Leu	Lys	Asn	Pro	Lys	Ile	Ala	Asp	Tyr	Leu	Thr	Arg
1				5					10					15
Tyr	Glu	His	Phe	Ser	Ser	Cys	Leu	His	Gln	Val	Leu	Gly	Leu	Leu
				20					25					30
Asn	Gly	Lys	Asp	Pro	Asp	Ser	Ser	Ser	Lys	Val	Leu	Glu	Leu	Leu
				35					40					45
Leu	Ala	Phe	Cys	Ser	Val	Thr	Gln	Leu	Arg	His	Met	Leu	Thr	Gln
				50					55					60
Met	Met	Phe	Glu	Gln	Ser	Pro	Pro	Gly	Ser	Ala	Thr	Leu	Gly	Ser
				65					70					75
His	Thr	Lys	Cys	Leu	Glu	Pro	Thr	Val	Ala	Leu	Leu	Arg	Trp	Leu
				80					85					90
Ser	Gln	Pro	Leu	Asp	Gly	Ser	Glu	Asn	Cys	Ser	Val	Leu	Ala	Leu
				95					100					105
Glu	Leu	Phe	Lys	Glu	Ile	Phe	Glu	Asp	Val	Ile	Asp	Ala	Ala	Asn
				110					115					120
Cys	Ser	Ser	Ala	Asp	Arg	Phe	Val	Thr	Leu	Leu	Leu	Pro	Thr	Ile
				125					130					135
Leu	Asp	Gln	Leu	Gln	Phe	Thr	Glu	Gln	Asn	Leu	Asp	Glu	Ala	Leu
				140					145					150
Thr	Arg	Gln	Lys	Cys	Glu	Arg	Ile	Ala	Lys	Ala	Phe	Glu	Val	Leu
				155					160					165
Leu	Thr	Leu	Cys	Gly	Asp	Asp	Thr	Leu	Lys	Met	His	Ile	Ala	Lys
				170					175					180
Ile	Leu	Thr	Thr	Val	Lys	Cys	Thr	Thr	Leu	Ile	Glu	Gln	Gln	Phe
				185					190					195
Thr	Tyr	Gly	Lys	Ile	Asp	Leu	Gly	Phe	Gly	Thr	Lys	Val	Ala	Asp
				200					205					210
Ser	Glu	Leu	Cys	Lys	Leu	Ala	Ala	Asp	Val	Ile	Leu	Lys	Thr	Leu
				215					220					225
Asp	Leu	Ile	Asn	Lys	Leu	Lys	Pro	Leu	Val	Pro	Gly	Met	Glu	Val
				230					235					240
Ser	Phe	Tyr	Lys	Ile	Leu	Gln	Asp	Pro	Arg	Leu	Ile	Thr	Pro	Leu
				245					250					255
Ala	Phe	Ala	Leu	Thr	Ser	Asp	Asn	Arg	Glu	Gln	Val	Gln	Ser	Gly

Leu Arg Ile Leu	260	Leu Glu Ala Ala Pro	265	Leu Pro Asp Phe Pro	270
Leu Val Leu Gly	275	Glu Ser Ile Ala Ala	280	Asn Asn Ala Tyr Arg	285
Gln Glu Thr Glu	290	His Ile Pro Arg Lys	295	Met Pro Trp Gln Ser	300
Asn His Ser Phe	305	Pro Thr Ser Ile Lys	310	Cys Leu Thr Pro His	315
Lys Asp Gly Val	320	Pro Gly Leu Asn Ile	325	Glu Glu Leu Ile Glu	330
Leu Gln Ser Gly	335	Met Val Val Lys Asp	340	Gln Ile Cys Asp Val	345
Ile Ser Asp Ile	350	Met Asp Val Tyr Glu	355	Met Lys Leu Ser Thr	360
Ala Ser Lys Glu	365	Ser Arg Leu Gln Asp	370	Leu Leu Glu Thr Lys	375
Leu Ala Leu Ala	380	Gln Ala Asp Arg Leu	385	Ile Ala Gln His Arg	390
Gln Arg Thr Gln	395	Ala Glu Thr Glu Ala	400	Arg Thr Leu Ala Ser	405
Leu Arg Glu Val	410	Glu Arg Lys Asn Glu	415	Glu Leu Ser Val Leu	420
Lys Ala Gln Gln	425	Val Glu Ser Glu Arg	430	Ala Gln Ser Asp Ile	435
His Leu Phe Gln	440	His Asn Arg Lys Leu	445	Glu Ser Val Ala Glu	450
His Glu Ile Leu	455	Thr Lys Ser Tyr Met	460	Glu Leu Leu Gln Arg	465
Glu Ser Thr Glu	470	Lys Lys Asn Lys Asp	475	Leu Gln Ile Thr Cys	480
Ser Leu Asn Lys	485	Gln Ile Glu Thr Val	490	Lys Lys Leu Asn Glu	495
Leu Lys Glu Gln	500	Asn Glu Lys Ser Ile	505	Ala Gln Leu Ile Glu	510
Glu Glu Gln Arg	515	Lys Glu Val Gln Asn	520	Gln Leu Val Asp Arg	525
His Lys Leu Ala	530	Asn Leu His Gln Lys	535	Thr Lys Val Gln Glu	540
Lys Ile Lys Thr	545	Leu Gln Lys Glu Arg	550	Glu Asp Lys Glu Glu	555
Ile Asp Ile Leu	560	Arg Lys Glu Leu Ser	565	Arg Thr Glu Gln Ile	570
Lys Glu Leu Ser	575	Ile Lys Ala Ser Ser	580	Leu Glu Val Gln Lys	585
Gln Leu Glu Gly	590	Arg Leu Glu Glu Lys	595	Glu Ser Leu Val Lys	600
Gln Gln Glu Glu	605	Leu Asn Lys His Ser	610	His Met Ile Ala Met	615
His Ser Leu Ser	620	Gly Gly Lys Ile Asn	625	Pro Glu Thr Val Asn	630
Ser Ile	635		640		645

<210> 9

<211> 1086

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2738233CD1

<400> 9

Met Arg Cys Lys	Glu Leu Glu Asn Ala Val	Gly Ser Trp Thr Asp
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Asp Leu Thr Gln	Leu Ser Leu Leu Lys Asp	Thr Leu Ser Ala Tyr

	20		25		30
Ile Ser Ala Asp	Asp	Ile Ser Ile Leu	Asn Glu Arg Val Glu	Leu	
	35		40		45
Leu Gln Arg Gln	Trp	Glu Glu Leu Cys	His Gln Leu Ser Leu	Arg	
	50		55		60
Arg Gln Gln Ile	Gly	Glu Arg Leu Asn	Glu Trp Ala Val Phe	Ser	
	65		70		75
Glu Lys Asn Lys	Glu	Leu Cys Glu Trp	Leu Thr Gln Met Glu	Ser	
	80		85		90
Lys Val Ser Gln	Asn	Gly Asp Ile Leu	Ile Glu Glu Met Ile	Glu	
	95		100		105
Lys Leu Lys Lys	Asp	Tyr Gln Glu Glu	Ile Ala Ile Ala Gln	Glu	
	110		115		120
Asn Lys Ile Gln	Leu	Gln Gln Met Gly	Glu Arg Leu Ala Lys	Ala	
	125		130		135
Ser His Glu Ser	Lys	Ala Ser Glu Ile	Glu Tyr Lys Leu Gly	Lys	
	140		145		150
Val Asn Asp Arg	Trp	Gln His Leu Leu	Asp Leu Ile Ala Ala	Arg	
	155		160		165
Val Lys Lys Leu	Lys	Glu Thr Leu Val	Ala Val Gln Gln Leu	Asp	
	170		175		180
Lys Asn Met Ser	Ser	Leu Arg Thr Trp	Leu Ala His Ile Glu	Ser	
	185		190		195
Glu Leu Ala Lys	Pro	Ile Val Tyr Gly	Ser Cys Asn Ser Glu	Glu	
	200		205		210
Ile Gln Arg Lys	Leu	Asn Glu Gln Gln	Glu Leu Gln Arg Asp	Ile	
	215		220		225
Glu Lys His Ser	Thr	Gly Val Ala Ser	Val Leu Asn Leu Cys	Glu	
	230		235		240
Val Leu Leu His	Asp	Cys Asp Ala Cys	Ala Thr Asp Ala Glu	Cys	
	245		250		255
Asp Ser Ile Gln	Gln	Ala Thr Arg Asn	Leu Asp Arg Arg Trp	Arg	
	260		265		270
Asn Ile Cys Ala	Met	Ser Met Glu Arg	Arg Leu Lys Ile Glu	Glu	
	275		280		285
Thr Trp Arg Leu	Trp	Gln Lys Phe Leu	Asp Asp Tyr Ser Arg	Phe	
	290		295		300
Glu Asp Trp Leu	Lys	Ser Ser Glu Arg	Thr Ala Ala Phe Pro	Ser	
	305		310		315
Ser Ser Gly Val	Ile	Tyr Thr Val Ala	Lys Glu Glu Leu Lys	Lys	
	320		325		330
Phe Glu Ala Phe	Gln	Arg Gln Val His	Glu Cys Leu Thr Gln	Leu	
	335		340		345
Glu Leu Ile Asn	Lys	Gln Tyr Arg Arg	Leu Ala Arg Glu Asn	Arg	
	350		355		360
Thr Asp Ser Ala	Cys	Ser Leu Lys Gln	Met Val His Glu Gly	Asn	
	365		370		375
Gln Arg Trp Asp	Asn	Leu Gln Lys Arg	Val Thr Ser Ile Leu	Arg	
	380		385		390
Arg Leu Lys His	Phe	Ile Gly Gln Arg	Glu Glu Phe Glu Thr	Ala	
	395		400		405
Arg Asp Ser Ile	Leu	Val Trp Leu Thr	Glu Met Asp Leu Gln	Leu	
	410		415		420
Thr Asn Ile Glu	His	Phe Ser Glu Cys	Asp Val Gln Ala Lys	Ile	
	425		430		435
Lys Gln Leu Lys	Ala	Phe Gln Gln Glu	Ile Ser Leu Asn His	Asn	
	440		445		450
Lys Ile Glu Gln	Ile	Ile Ala Gln Gly	Glu Gln Leu Ile Glu	Lys	
	455		460		465
Ser Glu Pro Leu	Asp	Ala Ala Ile Ile	Glu Glu Glu Leu Asp	Glu	
	470		475		480
Leu Arg Arg Tyr	Cys	Gln Glu Val Phe	Gly Arg Val Glu Arg	Tyr	
	485		490		495
His Lys Lys Leu	Ile	Arg Leu Pro Leu	Pro Asp Asp Glu His	Asp	
	500		505		510
Leu Ser Asp Arg	Glu	Leu Glu Leu Glu	Asp Ser Ala Ala Leu	Ser	
	515		520		525

Asp	Leu	His	Trp	His	Asp	Arg	Ser	Ala	Asp	Ser	Leu	Leu	Ser	Pro
				530					535					540
Gln	Pro	Ser	Ser	Asn	Leu	Ser	Leu	Ser	Leu	Ala	Gln	Pro	Leu	Arg
				545					550					555
Ser	Glu	Arg	Ser	Gly	Arg	Asp	Thr	Pro	Ala	Ser	Val	Asp	Ser	Ile
				560					565					570
Pro	Leu	Glu	Trp	Asp	His	Asp	Tyr	Asp	Leu	Ser	Arg	Asp	Leu	Glu
				575					580					585
Ser	Ala	Met	Ser	Arg	Ala	Leu	Pro	Ser	Glu	Asp	Glu	Glu	Gly	Gln
				590					595					600
Asp	Asp	Lys	Asp	Phe	Tyr	Leu	Arg	Gly	Ala	Val	Gly	Leu	Ser	Gly
				605					610					615
Asp	His	Ser	Ala	Leu	Glu	Ser	Gln	Ile	Arg	Gln	Leu	Gly	Lys	Ala
				620					625					630
Leu	Asp	Asp	Ser	Arg	Phe	Gln	Ile	Gln	Gln	Thr	Glu	Asn	Ile	Ile
				635					640					645
Arg	Ser	Lys	Thr	Pro	Thr	Gly	Pro	Glu	Leu	Asp	Thr	Ser	Tyr	Lys
				650					655					660
Gly	Tyr	Met	Lys	Leu	Leu	Gly	Glu	Cys	Ser	Ser	Ser	Ile	Asp	Ser
				665					670					675
Val	Lys	Arg	Leu	Glu	His	Lys	Leu	Lys	Glu	Glu	Glu	Glu	Ser	Leu
				680					685					690
Pro	Gly	Phe	Val	Asn	Leu	His	Ser	Thr	Glu	Thr	Gln	Thr	Ala	Gly
				695					700					705
Val	Ile	Asp	Arg	Trp	Glu	Leu	Leu	Gln	Ala	Gln	Ala	Leu	Ser	Lys
				710					715					720
Glu	Leu	Arg	Met	Lys	Gln	Asn	Leu	Gln	Lys	Trp	Gln	Gln	Phe	Asn
				725					730					735
Ser	Asp	Leu	Asn	Ser	Ile	Trp	Ala	Trp	Leu	Gly	Asp	Thr	Glu	Glu
				740					745					750
Glu	Leu	Glu	Gln	Leu	Gln	Arg	Leu	Glu	Leu	Ser	Thr	Asp	Ile	Gln
				755					760					765
Thr	Ile	Glu	Leu	Gln	Ile	Lys	Lys	Leu	Lys	Glu	Leu	Gln	Lys	Ala
				770					775					780
Val	Asp	His	Arg	Lys	Ala	Ile	Ile	Leu	Ser	Ile	Asn	Leu	Cys	Ser
				785					790					795
Pro	Glu	Phe	Thr	Gln	Ala	Asp	Ser	Lys	Glu	Ser	Arg	Asp	Leu	Gln
				800					805					810
Asp	Arg	Leu	Ser	Gln	Met	Asn	Gly	Arg	Trp	Asp	Arg	Val	Cys	Ser
				815					820					825
Leu	Leu	Glu	Glu	Trp	Arg	Gly	Leu	Leu	Gln	Asp	Ala	Leu	Met	Gln
				830					835					840
Cys	Gln	Gly	Phe	His	Glu	Met	Ser	His	Gly	Leu	Leu	Leu	Met	Leu
				845					850					855
Glu	Asn	Ile	Asp	Arg	Arg	Lys	Asn	Glu	Ile	Val	Pro	Ile	Asp	Ser
				860					865					870
Asn	Leu	Asp	Ala	Glu	Ile	Leu	Gln	Asp	His	His	Lys	Gln	Leu	Met
				875					880					885
Gln	Ile	Lys	His	Glu	Leu	Leu	Glu	Ser	Gln	Leu	Arg	Val	Ala	Ser
				890					895					900
Leu	Gln	Asp	Met	Ser	Cys	Gln	Leu	Leu	Val	Asn	Ala	Glu	Gly	Thr
				905					910					915
Asp	Cys	Leu	Glu	Ala	Lys	Glu	Lys	Val	His	Val	Ile	Gly	Asn	Arg
				920					925					930
Leu	Lys	Leu	Leu	Leu	Lys	Glu	Val	Ser	Arg	His	Ile	Lys	Glu	Leu
				935					940					945
Glu	Lys	Leu	Leu	Asp	Val	Ser	Ser	Ser	Gln	Gln	Asp	Leu	Ser	Ser
				950					955					960
Trp	Ser	Ser	Ala	Asp	Glu	Leu	Asp	Thr	Ser	Gly	Ser	Val	Ser	Pro
				965					970					975
Thr	Ser	Gly	Arg	Ser	Thr	Pro	Asn	Arg	Gln	Lys	Thr	Pro	Arg	Gly
				980					985					990
Lys	Cys	Ser	Leu	Ser	Gln	Pro	Gly	Pro	Ser	Val	Ser	Ser	Pro	His
				995					1000					1005
Ser	Arg	Ser	Thr	Lys	Gly	Gly	Ser	Asp	Ser	Ser	Leu	Ser	Glu	Pro
				1010					1015					1020
Gly	Pro	Gly	Arg	Ser	Gly	Arg	Gly	Phe	Leu	Phe	Arg	Val	Leu	Arg

1025	1030	1035
Ala Ala Leu Pro Leu	Gln Leu Leu Leu Leu	Leu Leu Ile Gly Leu
1040	1045	1050
Ala Cys Leu Val Pro	Met Ser Glu Glu Asp	Tyr Ser Cys Ala Leu
1055	1060	1065
Ser Asn Asn Phe Ala	Arg Ser Phe His Pro	Met Leu Arg Tyr Thr
1070	1075	1080
Asn Gly Pro Pro Pro	Leu	
1085		

<210> 10

<211> 396

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1833116CD1

<400> 10

Met Thr Thr Leu Val	Leu Asp Asn Gly Ala	Tyr Asn Ala Lys Ile
1	5	10
Gly Tyr Ser His	Glu Asn Val Ser Val	Ile Pro Asn Cys Gln Phe
20	25	30
Arg Ser Lys Thr	Ala Arg Leu Lys Thr	Phe Thr Ala Asn Gln Ile
35	40	45
Asp Glu Ile Lys	Asp Pro Ser Gly Leu	Phe Tyr Ile Leu Pro Phe
50	55	60
Gln Lys Gly Tyr	Leu Val Asn Trp Asp	Val Gln Arg Gln Val Trp
65	70	75
Asp Tyr Leu Phe	Gly Lys Glu Met Tyr	Gln Val Asp Phe Leu Asp
80	85	90
Thr Asn Ile Ile	Ile Thr Glu Pro Tyr	Phe Asn Phe Thr Ser Ile
95	100	105
Gln Glu Ser Met	Asn Glu Ile Leu Phe	Glu Tyr Gln Phe Gln
110	115	120
Ala Val Leu Arg	Val Asn Ala Gly Ala	Leu Ser Ala His Arg Tyr
125	130	135
Phe Arg Asp Asn	Pro Ser Glu Leu Cys	Cys Ile Ile Val Asp Ser
140	145	150
Gly Tyr Ser Phe	Thr His Ile Val Pro	Tyr Cys Arg Ser Lys Lys
155	160	165
Lys Lys Glu Ala	Ile Ile Arg Ile Asn	Val Gly Gly Lys Leu Leu
170	175	180
Thr Asn His Leu	Lys Glu Ile Ile Ser	Tyr Arg Gln Leu His Val
185	190	195
Met Asp Glu Thr	His Val Ile Asn Gln	Val Lys Glu Asp Val Cys
200	205	210
Tyr Val Ser Gln	Asp Phe Tyr Arg Asp	Met Asp Ile Ala Lys Leu
215	220	225
Lys Gly Glu Glu	Asn Thr Val Met Ile	Asp Tyr Val Leu Pro Asp
230	235	240
Phe Ser Thr Ile	Lys Lys Gly Phe Cys	Lys Pro Arg Glu Glu Met
245	250	255
Val Leu Ser Gly	Lys Tyr Lys Ser Gly	Glu Gln Ile Leu Arg Leu
260	265	270
Ala Asn Glu Arg	Phe Ala Val Pro Glu	Ile Leu Phe Asn Pro Ser
275	280	285
Asp Ile Gly Ile	Gln Glu Met Gly Ile	Pro Glu Ala Ile Val Tyr
290	295	300
Ser Ile Gln Asn	Leu Pro Glu Glu Met	Gln Pro His Phe Phe Lys
305	310	315
Asn Ile Val Leu	Thr Gly Gly Asn Ser	Leu Phe Pro Gly Phe Arg
320	325	330
Asp Arg Val Tyr	Ser Glu Val Arg Cys	Leu Thr Pro Thr Asp Tyr
335	340	345
Asp Val Ser Val	Val Leu Pro Glu Asn	Pro Ile Thr Tyr Ala Trp

	350		355		360
Glu Gly Gly Lys	Leu Ile Ser Glu Asn Asp	Asp Phe Glu Asp	Met		
	365		370		375
Val Val Thr Arg	Glu Asp Tyr Glu Glu Asn	Gly His Ser Val	Cys		
	380		385		390
Glu Glu Lys Phe	Asp Ile				
	395				

<210> 11
 <211> 304
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 001799CD1

<400> 11

Met	Ala	Ser	Glu	Thr	His	Asn	Val	Lys	Lys	Arg	Asn	Phe	Cys	Asn
1				5					10					15
Lys	Ile	Glu	Asp	His	Phe	Ile	Asp	Leu	Pro	Arg	Lys	Lys	Ile	Ser
				20					25					30
Asn	Phe	Thr	Asn	Lys	Asn	Met	Lys	Glu	Val	Lys	Lys	Ser	Pro	Lys
				35					40					45
Gln	Leu	Ala	Ala	Tyr	Ile	Asn	Arg	Thr	Val	Gly	Gln	Thr	Val	Lys
				50					55					60
Ser	Pro	Asp	Lys	Leu	Arg	Lys	Val	Ile	Tyr	Arg	Arg	Lys	Lys	Val
				65					70					75
His	His	Pro	Phe	Pro	Asn	Pro	Cys	Tyr	Arg	Lys	Lys	Gln	Ser	Pro
				80					85					90
Gly	Ser	Gly	Gly	Cys	Asp	Met	Ala	Asn	Lys	Glu	Asn	Glu	Leu	Ala
				95					100					105
Cys	Ala	Gly	His	Leu	Pro	Glu	Lys	Leu	His	His	Asp	Ser	Arg	Thr
				110					115					120
Tyr	Leu	Val	Asn	Ser	Ser	Asp	Ser	Gly	Ser	Ser	Gln	Thr	Glu	Ser
				125					130					135
Pro	Ser	Ser	Lys	Tyr	Ser	Gly	Phe	Phe	Ser	Glu	Val	Ser	Gln	Asp
				140					145					150
His	Glu	Thr	Met	Ala	Gln	Val	Leu	Phe	Ser	Arg	Asn	Met	Arg	Leu
				155					160					165
Asn	Val	Ala	Leu	Thr	Phe	Trp	Arg	Lys	Arg	Ser	Ile	Ser	Glu	Leu
				170					175					180
Val	Ala	Tyr	Leu	Leu	Arg	Ile	Glu	Asp	Leu	Gly	Val	Val	Val	Asp
				185					190					195
Cys	Leu	Pro	Val	Leu	Thr	Asn	Cys	Leu	Gln	Glu	Glu	Lys	Gln	Tyr
				200					205					210
Ile	Ser	Leu	Gly	Cys	Cys	Val	Asp	Leu	Leu	Pro	Leu	Val	Lys	Ser
				215					220					225
Leu	Leu	Lys	Ser	Lys	Phe	Glu	Glu	Tyr	Val	Ile	Val	Gly	Leu	Asn
				230					235					240
Trp	Leu	Gln	Ala	Val	Ile	Lys	Arg	Trp	Trp	Ser	Glu	Leu	Ser	Ser
				245					250					255
Lys	Thr	Glu	Ile	Ile	Asn	Asp	Gly	Asn	Ile	Gln	Ile	Leu	Lys	Gln
				260					265					270
Gln	Leu	Ser	Gly	Leu	Trp	Glu	Gln	Glu	Asn	His	Leu	Thr	Leu	Val
				275					280					285
Pro	Gly	Tyr	Thr	Gly	Asn	Ile	Ala	Lys	Asp	Val	Asp	Ala	Tyr	Leu
				290					295					300
Leu	Gln	Leu	His											

<210> 12
 <211> 201
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc_feature
 <223> Incyte ID No: 119814CD1

<400> 12

Met	Ile	Val	Ser	Glu	Lys	Gly	Leu	His	Ser	Leu	Ile	Phe	Glu	Val	
1				5					10					15	
Val	Arg	Ala	Ser	Asp	Ala	Gly	Ala	Tyr	Ala	Cys	Val	Ala	Lys	Asn	
				20					25					30	
Arg	Ala	Gly	Glu	Ala	Thr	Phe	Thr	Val	Gln	Leu	Asp	Val	Leu	Ala	
				35					40					45	
Lys	Glu	His	Lys	Arg	Ala	Pro	Met	Phe	Ile	Tyr	Lys	Pro	Gln	Ser	
				50					55					60	
Lys	Lys	Val	Leu	Glu	Gly	Asp	Ser	Val	Lys	Leu	Glu	Cys	Gln	Ile	
				65					70					75	
Ser	Ala	Ile	Pro	Pro	Pro	Lys	Leu	Phe	Trp	Lys	Arg	Asn	Asn	Glu	
				80					85					90	
Met	Val	Gln	Phe	Asn	Thr	Asp	Arg	Ile	Ser	Leu	Tyr	Gln	Asp	Asn	
				95					100					105	
Thr	Gly	Arg	Val	Thr	Leu	Leu	Ile	Lys	Asp	Val	Asn	Lys	Lys	Asp	
				110					115					120	
Ala	Gly	Trp	Tyr	Thr	Val	Ser	Ala	Val	Asn	Glu	Ala	Gly	Val	Thr	
				125					130					135	
Thr	Cys	Asn	Thr	Arg	Leu	Asp	Val	Thr	Ala	Arg	Pro	Asn	Gln	Thr	
				140					145					150	
Leu	Pro	Ala	Pro	Lys	Gln	Leu	Arg	Val	Arg	Pro	Thr	Phe	Ser	Lys	
				155					160					165	
Tyr	Leu	Ala	Leu	Asn	Gly	Lys	Gly	Leu	Asn	Val	Lys	Gln	Ala	Phe	
				170					175					180	
Asn	Pro	Glu	Gly	Glu	Phe	Gln	Arg	Leu	Ala	Ala	Gln	Ser	Gly	Leu	
				185					190					195	
Tyr	Glu	Ser	Glu	Glu	Leu										
				200											

<210> 13

<211> 547

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1295420CD1

<400> 13

Met	Thr	Lys	Thr	Asp	Pro	Ala	Pro	Met	Ala	Pro	Pro	Pro	Arg	Gly	
1				5					10					15	
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Pro	Val	Pro	Glu	Ala	
				20					25					30	
Pro	Ser	Pro	Thr	Gln	Glu	Arg	Arg	Gln	Lys	Pro	Val	Val	His	Pro	
				35					40					45	
Ser	Ala	Pro	Ala	Pro	Leu	Pro	Lys	Asp	Tyr	Ala	Phe	Thr	Phe	Phe	
				50					55					60	
Asp	Pro	Asn	Asp	Pro	Ala	Cys	Gln	Glu	Ile	Leu	Phe	Asp	Pro	Gln	
				65					70					75	
Thr	Thr	Ile	Pro	Glu	Leu	Phe	Ala	Ile	Val	Arg	Gln	Trp	Val	Pro	
				80					85					90	
Gln	Val	Gln	His	Lys	Ile	Asp	Val	Ile	Gly	Asn	Glu	Ile	Leu	Arg	
				95					100					105	
Arg	Gly	Cys	His	Val	Asn	Asp	Arg	Asp	Gly	Leu	Thr	Asp	Met	Thr	
				110					115					120	
Leu	Leu	His	Tyr	Ala	Cys	Lys	Ala	Gly	Ala	His	Gly	Val	Gly	Asp	
				125					130					135	
Pro	Ala	Ala	Ala	Val	Arg	Leu	Ser	Gln	Gln	Leu	Leu	Ala	Leu	Gly	
				140					145					150	
Ala	Asp	Val	Thr	Leu	Arg	Ser	Arg	Trp	Thr	Asn	Met	Asn	Ala	Leu	
				155					160					165	
His	Tyr	Ala	Ala	Tyr	Phe	Asp	Val	Pro	Asp	Leu	Val	Arg	Val	Leu	
				170					175					180	


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Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp
185 190 195
Phe Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Ser Leu Cys
200 205 210
Leu Gly Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala
215 220 225
Leu Arg Asn Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp
230 235 240
Pro Met Asp Met Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala
245 250 255
Lys Glu Leu Arg Thr Leu Leu Glu Glu Ala Val Pro Leu Ser Cys
260 265 270
Ala Leu Pro Lys Val Thr Leu Pro Asn Tyr Asp Asn Val Pro Gly
275 280 285
Asn Leu Met Leu Ser Ala Leu Gly Leu Arg Leu Gly Asp Arg Val
290 295 300
Leu Leu Asp Gly Gln Lys Thr Gly Thr Leu Arg Phe Cys Gly Thr
305 310 315
Thr Glu Phe Ala Ser Gly Gln Trp Val Gly Val Glu Leu Asp Glu
320 325 330
Pro Glu Gly Lys Asn Asp Gly Ser Val Gly Gly Val Arg Tyr Phe
335 340 345
Ile Cys Pro Pro Lys Gln Gly Leu Phe Ala Ser Val Ser Lys Ile
350 355 360
Ser Lys Ala Val Asp Ala Pro Pro Ser Ser Val Thr Ser Thr Pro
365 370 375
Arg Thr Pro Arg Met Asp Phe Ser Arg Val Thr Gly Lys Gly Arg
380 385 390
Arg Glu His Lys Gly Lys Lys Lys Thr Pro Ser Ser Pro Ser Leu
395 400 405
Gly Ser Leu Gln Gln Arg Asp Gly Ala Lys Ala Glu Val Gly Asp
410 415 420
Gln Val Leu Val Ala Gly Gln Lys Gln Gly Ile Val Arg Phe Tyr
425 430 435
Gly Lys Thr Asp Phe Ala Pro Gly Tyr Trp Tyr Gly Ile Glu Leu
440 445 450
Asp Gln Pro Thr Gly Lys His Asp Gly Ser Val Phe Gly Val Arg
455 460 465
Tyr Phe Thr Cys Pro Pro Arg His Gly Val Phe Ala Pro Ala Ser
470 475 480
Arg Ile Gln Arg Ile Gly Gly Ser Thr Asp Ser Pro Gly Asp Ser
485 490 495
Val Gly Ala Lys Lys Val His Gln Val Thr Met Thr Gln Pro Lys
500 505 510
Arg Thr Phe Thr Thr Val Arg Thr Pro Lys Asp Ile Ala Ser Glu
515 520 525
Asn Ser Ile Ser Arg Leu Leu Phe Cys Cys Trp Phe Pro Trp Met
530 535 540
Leu Arg Ala Glu Met Gln Ser
545

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<210> 14

<211> 464

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1309364CD1

<400> 14

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Met Glu Thr Leu Ser Phe Pro Arg Tyr Asn Val Ala Glu Ile Val
1 5 10 15
Ile His Ile Arg Asn Lys Ile Leu Thr Gly Ala Asp Gly Lys Asn
20 25 30
Leu Thr Lys Asn Asp Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu
35 40 45

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His	Met	Ile	Tyr	Met	Arg	Ala	Leu	Gln	Ile	Val	Tyr	Gly	Ile	Arg
				50					55					60
Leu	Glu	His	Phe	Tyr	Met	Met	Pro	Val	Asn	Ser	Glu	Val	Met	Tyr
				65					70					75
Pro	His	Leu	Met	Glu	Gly	Phe	Leu	Pro	Phe	Ser	Asn	Leu	Val	Thr
				80					85					90
His	Leu	Asp	Ser	Phe	Leu	Pro	Ile	Cys	Arg	Val	Asn	Asp	Phe	Glu
				95					100					105
Thr	Ala	Asp	Ile	Leu	Cys	Pro	Lys	Ala	Lys	Arg	Thr	Ser	Arg	Phe
				110					115					120
Leu	Ser	Gly	Ile	Ile	Asn	Phe	Ile	His	Phe	Arg	Glu	Ala	Cys	Arg
				125					130					135
Glu	Thr	Tyr	Met	Glu	Phe	Leu	Trp	Gln	Tyr	Lys	Ser	Ser	Ala	Asp
				140					145					150
Lys	Met	Gln	Gln	Leu	Asn	Ala	Ala	His	Gln	Glu	Ala	Leu	Met	Lys
				155					160					165
Leu	Glu	Arg	Leu	Asp	Ser	Val	Pro	Val	Glu	Glu	Gln	Glu	Glu	Phe
				170					175					180
Lys	Gln	Leu	Ser	Asp	Gly	Ile	Gln	Glu	Leu	Gln	Gln	Ser	Leu	Asn
				185					190					195
Gln	Asp	Phe	His	Gln	Lys	Thr	Ile	Val	Leu	Gln	Glu	Gly	Asn	Pro
				200					205					210
Gln	Lys	Lys	Ser	Asn	Ile	Ser	Glu	Lys	Thr	Lys	Arg	Leu	Asn	Glu
				215					220					225
Leu	Lys	Leu	Leu	Val	Val	Ser	Leu	Lys	Glu	Ile	Gln	Glu	Ser	Leu
				230					235					240
Lys	Thr	Lys	Ile	Val	Asp	Ser	Pro	Glu	Lys	Leu	Lys	Asn	Tyr	Lys
				245					250					255
Glu	Lys	Met	Lys	Asp	Thr	Val	Gln	Lys	Leu	Lys	Asn	Ala	Arg	Gln
				260					265					270
Glu	Val	Val	Glu	Lys	Tyr	Glu	Ile	Tyr	Gly	Asp	Ser	Val	Asp	Cys
				275					280					285
Leu	Pro	Ser	Cys	Gln	Leu	Glu	Val	Gln	Leu	Tyr	Gln	Lys	Lys	Ile
				290					295					300
Gln	Asp	Leu	Ser	Asp	Asn	Arg	Glu	Lys	Leu	Ala	Ser	Ile	Leu	Lys
				305					310					315
Glu	Ser	Leu	Asn	Leu	Glu	Asp	Gln	Ile	Glu	Ser	Asp	Glu	Ser	Glu
				320					325					330
Leu	Lys	Lys	Leu	Lys	Thr	Glu	Glu	Asn	Ser	Phe	Lys	Arg	Leu	Met
				335					340					345
Ile	Val	Lys	Lys	Glu	Lys	Leu	Ala	Thr	Ala	Gln	Phe	Lys	Ile	Asn
				350					355					360
Lys	Lys	His	Glu	Asp	Val	Lys	Gln	Tyr	Lys	Arg	Thr	Val	Ile	Glu
				365					370					375
Asp	Cys	Asn	Lys	Val	Gln	Glu	Lys	Arg	Gly	Ala	Val	Tyr	Glu	Arg
				380					385					390
Val	Thr	Thr	Ile	Asn	Gln	Glu	Ile	Gln	Lys	Ile	Lys	Leu	Gly	Ile
				395					400					405
Gln	Gln	Leu	Lys	Asp	Ala	Ala	Glu	Arg	Glu	Lys	Leu	Lys	Ser	Gln
				410					415					420
Glu	Ile	Phe	Leu	Asn	Leu	Lys	Thr	Ala	Leu	Glu	Lys	Tyr	His	Asp
				425					430					435
Gly	Ile	Glu	Lys	Ala	Ala	Glu	Asp	Ser	Tyr	Ala	Lys	Ile	Asp	Glu
				440					445					450
Lys	Thr	Ala	Glu	Leu	Lys	Arg	Lys	Met	Phe	Lys	Met	Ser	Thr	
				455					460					

<210> 15

<211> 569

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1315267CD1

<400> 15

Met	Glu	Ser	Ile	Lys	His	Lys	Val	Ser	Glu	Pro	Ser	Arg	Ser	Ser
1				5					10					15
Ser	Leu	Ser	Leu	Ser	Lys	Met	Asp	Phe	Asp	Asp	Glu	Arg	Thr	Trp
				20					25					30
Thr	Asp	Leu	Glu	Glu	Asn	Leu	Cys	Asn	His	Asp	Val	Val	Leu	Gly
				35					40					45
Asn	Glu	Ser	Thr	Tyr	Gly	Thr	Pro	Gln	Thr	Cys	Tyr	Pro	Asn	Asn
				50					55					60
Glu	Ile	Gly	Ile	Leu	Asp	Lys	Thr	Ile	Lys	Arg	Lys	Ile	Ala	Pro
				65					70					75
Val	Lys	Arg	Gly	Glu	Asp	Leu	Ser	Lys	Ser	Arg	Arg	Ser	Arg	Ser
				80					85					90
Pro	Pro	Thr	Ser	Glu	Leu	Met	Met	Lys	Phe	Phe	Pro	Ser	Leu	Lys
				95					100					105
Pro	Lys	Pro	Lys	Ser	Asp	Ser	His	Leu	Gly	Asn	Glu	Leu	Lys	Leu
				110					115					120
Asn	Ile	Ser	Gln	Asp	Gln	Pro	Pro	Gly	Asp	Asn	Ala	Arg	Ser	Gln
				125					130					135
Val	Leu	Arg	Glu	Lys	Ile	Ile	Glu	Leu	Glu	Thr	Glu	Ile	Glu	Lys
				140					145					150
Phe	Lys	Ala	Glu	Asn	Ala	Ser	Leu	Ala	Lys	Leu	Arg	Ile	Glu	Arg
				155					160					165
Glu	Ser	Ala	Leu	Glu	Lys	Leu	Arg	Lys	Glu	Ile	Ala	Asp	Phe	Glu
				170					175					180
Gln	Gln	Lys	Ala	Lys	Glu	Leu	Ala	Arg	Ile	Glu	Glu	Phe	Lys	Lys
				185					190					195
Glu	Glu	Met	Arg	Lys	Leu	Gln	Lys	Glu	Arg	Lys	Val	Phe	Glu	Lys
				200					205					210
Tyr	Thr	Thr	Ala	Ala	Arg	Thr	Phe	Pro	Asp	Lys	Lys	Glu	Arg	Glu
				215					220					225
Glu	Ile	Gln	Thr	Leu	Lys	Gln	Gln	Ile	Ala	Asp	Leu	Arg	Glu	Asp
				230					235					240
Leu	Lys	Arg	Lys	Glu	Thr	Lys	Trp	Ser	Ser	Thr	His	Ser	Arg	Leu
				245					250					255
Arg	Ser	Gln	Ile	Gln	Met	Leu	Val	Arg	Glu	Asn	Thr	Asp	Leu	Arg
				260					265					270
Glu	Glu	Ile	Lys	Val	Met	Glu	Arg	Phe	Arg	Leu	Asp	Ala	Trp	Lys
				275					280					285
Arg	Ala	Glu	Ala	Ile	Glu	Ser	Ser	Leu	Glu	Val	Glu	Lys	Lys	Asp
				290					295					300
Lys	Leu	Ala	Asn	Thr	Ser	Val	Arg	Phe	Gln	Asn	Ser	Gln	Ile	Ser
				305					310					315
Ser	Gly	Thr	Gln	Val	Glu	Lys	Tyr	Lys	Lys	Asn	Tyr	Leu	Pro	Met
				320					325					330
Gln	Gly	Asn	Pro	Pro	Arg	Arg	Ser	Lys	Ser	Ala	Pro	Pro	Arg	Asp
				335					340					345
Leu	Gly	Asn	Leu	Asp	Lys	Gly	Gln	Ala	Ala	Ser	Pro	Arg	Glu	Pro
				350					355					360
Leu	Glu	Pro	Leu	Asn	Phe	Pro	Asp	Pro	Glu	Tyr	Lys	Glu	Glu	Glu
				365					370					375
Glu	Asp	Gln	Asp	Ile	Gln	Gly	Glu	Ile	Ser	His	Pro	Asp	Gly	Lys
				380					385					390
Val	Glu	Lys	Val	Tyr	Lys	Asn	Gly	Cys	Arg	Val	Ile	Leu	Phe	Pro
				395					400					405
Asn	Gly	Thr	Arg	Lys	Glu	Val	Ser	Ala	Asp	Gly	Lys	Thr	Ile	Thr
				410					415					420
Val	Thr	Phe	Phe	Asn	Gly	Asp	Val	Lys	Gln	Val	Met	Pro	Asp	Gln
				425					430					435
Arg	Val	Ile	Tyr	Tyr	Tyr	Ala	Ala	Ala	Gln	Thr	Thr	His	Thr	Thr
				440					445					450
Tyr	Pro	Glu	Gly	Leu	Glu	Val	Leu	His	Phe	Ser	Ser	Gly	Gln	Ile
				455					460					465
Glu	Lys	His	Tyr	Pro	Asp	Gly	Arg	Lys	Glu	Ile	Thr	Phe	Pro	Asp
				470					475					480
Gln	Thr	Val	Lys	Asn	Leu	Phe	Pro	Asp	Gly	Gln	Glu	Glu	Ser	Ile
				485					490					495
Phe	Pro	Asp	Gly	Thr	Ile	Val	Arg	Val	Gln	Arg	Asp	Gly	Asn	Lys

Leu	Ile	Glu	Phe	Asn	Asn	Gly	Gln	Arg	Glu	Leu	His	Thr	Ala	Gln
				515					520					525
Phe	Lys	Arg	Arg	Glu	Tyr	Pro	Asp	Gly	Thr	Val	Lys	Thr	Val	Tyr
				530					535					540
Ala	Asn	Gly	His	Gln	Glu	Thr	Lys	Tyr	Arg	Ser	Gly	Arg	Ile	Arg
				545					550					555
Val	Lys	Asp	Lys	Glu	Gly	Asn	Val	Leu	Met	Asp	Thr	Glu	Leu	
				560					565					

<210> 16
 <211> 436
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1403289CD1

<400> 16

Met	Leu	Leu	Ser	Pro	Lys	Phe	Ser	Leu	Ser	Thr	Ile	His	Ile	Arg
1				5					10					15
Leu	Thr	Ala	Lys	Gly	Leu	Leu	Arg	Asn	Leu	Arg	Leu	Pro	Ser	Gly
				20					25					30
Phe	Arg	Arg	Ser	Thr	Val	Val	Phe	His	Thr	Val	Glu	Lys	Ser	Arg
				35					40					45
Gln	Lys	Asn	Pro	Arg	Ser	Leu	Cys	Ile	Gln	Pro	Gln	Thr	Ala	Pro
				50					55					60
Asp	Ala	Leu	Pro	Pro	Glu	Lys	Thr	Leu	Glu	Leu	Thr	Gln	Tyr	Lys
				65					70					75
Thr	Lys	Cys	Glu	Asn	Gln	Ser	Gly	Phe	Ile	Leu	Gln	Leu	Lys	Gln
				80					85					90
Leu	Leu	Ala	Cys	Gly	Asn	Thr	Lys	Phe	Glu	Ala	Leu	Thr	Val	Val
				95					100					105
Ile	Gln	His	Leu	Leu	Ser	Glu	Arg	Glu	Glu	Ala	Leu	Lys	Gln	His
				110					115					120
Lys	Thr	Leu	Ser	Gln	Glu	Leu	Val	Asn	Leu	Arg	Gly	Glu	Leu	Val
				125					130					135
Thr	Ala	Ser	Thr	Thr	Cys	Glu	Lys	Leu	Glu	Lys	Ala	Arg	Asn	Glu
				140					145					150
Leu	Gln	Thr	Val	Tyr	Glu	Ala	Phe	Val	Gln	Gln	His	Gln	Ala	Glu
				155					160					165
Lys	Thr	Glu	Arg	Glu	Asn	Arg	Leu	Lys	Glu	Phe	Tyr	Thr	Arg	Glu
				170					175					180
Tyr	Glu	Lys	Leu	Arg	Asp	Thr	Tyr	Ile	Glu	Glu	Ala	Glu	Lys	Tyr
				185					190					195
Lys	Met	Gln	Leu	Gln	Glu	Gln	Phe	Asp	Asn	Leu	Asn	Ala	Ala	His
				200					205					210
Glu	Thr	Ser	Lys	Leu	Glu	Ile	Glu	Ala	Ser	His	Ser	Glu	Lys	Leu
				215					220					225
Glu	Leu	Leu	Lys	Lys	Ala	Tyr	Glu	Ala	Ser	Leu	Ser	Glu	Ile	Lys
				230					235					240
Lys	Gly	His	Glu	Ile	Glu	Lys	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Ser
				245					250					255
Glu	Lys	Gln	Glu	Ser	Leu	Glu	Lys	Gln	Ile	Asn	Asp	Leu	Lys	Ser
				260					265					270
Glu	Asn	Asp	Ala	Leu	Asn	Glu	Lys	Leu	Lys	Ser	Glu	Glu	Gln	Lys
				275					280					285
Arg	Arg	Ala	Arg	Glu	Lys	Ala	Asn	Leu	Lys	Asn	Pro	Gln	Ile	Met
				290					295					300
Tyr	Leu	Glu	Gln	Glu	Leu	Glu	Ser	Leu	Lys	Ala	Val	Leu	Glu	Ile
				305					310					315
Lys	Asn	Glu	Lys	Leu	His	Gln	Gln	Asp	Ile	Lys	Leu	Met	Lys	Met
				320					325					330
Glu	Lys	Leu	Val	Asp	Asn	Asn	Thr	Ala	Leu	Val	Asp	Lys	Leu	Lys
				335					340					345
Arg	Phe	Gln	Gln	Glu	Asn	Glu	Glu	Leu	Lys	Ala	Arg	Met	Asp	Lys

His Met Ala Ile	350	Ser Arg Gln Leu Ser	355	Thr Glu Gln Ala Val	360
	365		370		375
Gln Glu Ser Leu	380	Glu Lys Glu Ser Lys	385	Val Asn Lys Arg Leu	390
	395		400		405
Met Glu Asn Glu	410	Leu Leu Trp Lys	415	Leu His Asn Gly Asp	420
	425		430		435
Cys Ser Pro Lys		Arg Ser Pro Thr Ser		Ser Ala Ile Pro Leu	
Ser Pro Arg Asn		Ser Gly Ser Leu His		Ser Pro Ser Ile Ser	
Arg					

<210> 17
 <211> 363
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1607607CD1

<400> 17

Met Ala Ser Ala	Glu Leu Gln Gly	Lys Tyr Gln Lys	Leu Ala Gln
1	5	10	15
Glu Tyr Ser Lys	Leu Arg Ala Gln	Asn Gln Val Leu	Lys Lys Gly
	20	25	30
Val Val Asp Glu	Gln Ala Asn Ser	Ala Ala Leu Lys	Glu Gln Leu
	35	40	45
Lys Met Lys Asp	Gln Ser Leu Arg	Lys Leu Gln Gln	Glu Met Asp
	50	55	60
Ser Leu Thr Phe	Arg Asn Leu Gln	Leu Ala Lys Arg	Val Glu Leu
	65	70	75
Leu Gln Asp Glu	Leu Ala Leu Ser	Glu Pro Arg Gly	Lys Lys Asn
	80	85	90
Lys Lys Ser Gly	Glu Ser Ser Ser	Gln Leu Ser Gln	Glu Gln Lys
	95	100	105
Ser Val Phe Asp	Glu Asp Leu Gln	Lys Lys Ile Glu	Glu Asn Glu
	110	115	120
Arg Leu His Ile	Gln Phe Phe Glu	Ala Asp Glu Gln	His Lys His
	125	130	135
Val Glu Ala Glu	Leu Arg Ser Arg	Leu Ala Thr Leu	Glu Thr Glu
	140	145	150
Ala Ala Gln His	Gln Ala Val Val	Asp Gly Leu Thr	Arg Lys Tyr
	155	160	165
Met Glu Thr Ile	Glu Lys Leu Gln	Asn Asp Lys Ala	Lys Leu Glu
	170	175	180
Val Lys Ser Gln	Thr Leu Glu Lys	Glu Ala Lys Glu	Cys Arg Leu
	185	190	195
Arg Thr Glu Glu	Cys Gln Leu Gln	Leu Lys Thr Leu	His Glu Asp
	200	205	210
Leu Ser Gly Arg	Leu Glu Glu Ser	Leu Ser Ile Ile	Asn Glu Lys
	215	220	225
Val Pro Phe Asn	Asp Thr Lys Tyr	Ser Gln Tyr Asn	Ala Leu Asn
	230	235	240
Val Pro Leu His	Asn Arg Arg His	Gln Leu Lys Met	Arg Asp Ile
	245	250	255
Ala Gly Gln Ala	Leu Ala Phe Val	Gln Asp Leu Val	Thr Ala Leu
	260	265	270
Leu Asn Phe His	Thr Tyr Thr Glu	Gln Arg Ile Gln	Ile Phe Pro
	275	280	285
Val Asp Ser Ala	Ile Asp Thr Ile	Ser Pro Leu Asn	Gln Lys Phe
	290	295	300
Ser Gln Tyr Leu	His Glu Asn Ala	Ser Tyr Val Arg	Pro Leu Glu
	305	310	315
Glu Gly Met Leu	His Leu Phe Glu	Ser Ile Thr Glu	Asp Thr Val

				320					325					330
Thr	Vai	Leu	Glu	Thr	Thr	Vai	Lys	Leu	Lys	Thr	Phe	Ser	Glu	His
				335					340					345
Leu	Thr	Ser	Tyr	Ile	Cys	Phe	Leu	Arg	Lys	Ile	Leu	Pro	Tyr	Gln
				350					355					360
Leu	Lys	Arg												

<210> 18
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1660025CD1

<400> 18														
Met	Gly	Lys	Arg	Asp	Asn	Arg	Val	Ala	Tyr	Met	Asn	Pro	Ile	Ala
1				5					10					15
Met	Ala	Arg	Ser	Arg	Gly	Pro	Ile	Gln	Ser	Ser	Gly	Pro	Thr	Ile
				20					25					30
Gln	Asp	Tyr	Leu	Asn	Arg	Pro	Arg	Pro	Thr	Trp	Glu	Glu	Val	Lys
				35					40					45
Glu	Gln	Leu	Glu	Lys	Lys	Lys	Lys	Gly	Ser	Lys	Ala	Leu	Ala	Glu
				50					55					60
Phe	Glu	Glu	Lys	Met	Asn	Glu	Asn	Trp	Lys	Lys	Glu	Leu	Glu	Lys
				65					70					75
His	Arg	Glu	Lys	Leu	Leu	Ser	Gly	Ser	Glu	Ser	Ser	Ser	Lys	Lys
				80					85					90
Arg	Gln	Arg	Lys	Lys	Lys	Glu	Lys	Lys	Lys	Ser	Gly	Arg	Tyr	Ser
				95					100					105
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Asp
				110					115					120
Ser	Glu	Asp	Glu	Asp	Lys	Lys	Gln	Gly	Lys	Arg	Arg	Lys	Lys	Lys
				125					130					135
Lys	Asn	Arg	Ser	His	Lys	Ser	Ser	Glu	Ser	Ser	Met	Ser	Glu	Thr
				140					145					150
Glu	Ser	Asp	Ser	Lys	Asp	Ser	Leu	Lys	Lys	Lys	Lys	Lys	Ser	Lys
				155					160					165
Asp	Gly	Thr	Glu	Lys	Glu	Lys	Asp	Ile	Lys	Gly	Leu	Ser	Lys	Lys
				170					175					180
Arg	Lys	Met	Tyr	Ser	Glu	Asp	Lys	Pro	Leu	Ser	Ser	Glu	Ser	Leu
				185					190					195
Ser	Glu	Ser	Glu	Tyr	Ile	Glu	Glu	Val	Arg	Ala	Lys	Lys	Lys	Lys
				200					205					210
Ser	Ser	Glu	Glu	Arg	Glu	Lys	Ala	Thr	Glu	Lys	Thr	Lys	Lys	Lys
				215					220					225
Lys	Lys	His	Lys	Lys	His	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Ala	Ala
				230					235					240
Ser	Ser	Ser	Pro	Asp	Ser	Pro								
				245										

<210> 19
 <211> 441
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1796836CD1

<400> 19														
Met	Asp	Asp	Asp	Asp	Phe	Gly	Gly	Phe	Glu	Ala	Ala	Glu	Thr	Phe
1				5					10					15
Asp	Gly	Gly	Ser	Gly	Glu	Thr	Gln	Thr	Thr	Ser	Pro	Ala	Ile	Pro
				20					25					30

Met	Ala	Ala	Gln	Arg	Gly	Met	Pro	Ser	Ser	Ala	Val	Arg	Val	Leu	
1				5					10					15	
Glu	Glu	Ala	Leu	Gly	Met	Gly	Leu	Thr	Ala	Ala	Gly	Asp	Ala	Arg	
			20						25					30	
Asp	Thr	Ala	Asp	Ala	Val	Ala	Ala	Glu	Gly	Ala	Tyr	Tyr	Leu	Glu	
			35						40					45	
Gln	Val	Thr	Ile	Thr	Glu	Ala	Ser	Glu	Asp	Asp	Tyr	Glu	Tyr	Glu	
			50						55					60	
Glu	Ile	Pro	Asp	Asp	Asn	Phe	Ser	Ile	Pro	Glu	Gly	Glu	Glu	Asp	
			65						70					75	
Leu	Ala	Lys	Ala	Ile	Gln	Met	Ala	Gln	Glu	Gln	Ala	Thr	Asp	Thr	
			80						85					90	
Glu	Ile	Leu	Glu	Arg	Lys	Thr	Val	Leu	Pro	Ser	Lys	His	Ala	Val	
			95						100					105	
Pro	Glu	Val	Ile	Glu	Asp	Phe	Leu	Cys	Asn	Phe	Leu	Ile	Lys	Met	
			110						115					120	
Gly	Met	Thr	Arg	Thr	Leu	Asp	Cys	Phe	Gln	Ser	Glu	Trp	Tyr	Glu	
			125						130					135	
Leu	Ile	Gln	Lys	Gly	Val	Thr	Glu	Leu	Arg	Thr	Val	Gly	Asn	Val	
			140						145					150	
Pro	Asp	Val	Tyr	Thr	Gln	Ile	Met	Leu	Leu	Glu	Asn	Glu	Asn	Lys	
			155						160					165	
Asn	Leu	Lys	Lys	Asp	Leu	Lys	His	Tyr	Lys	Gln	Ala	Ala	Glu	Tyr	
			170						175					180	
Val	Ile	Phe													

<210> 21

<211> 212

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2913976CD1

<400> 21

Met	Glu	Glu	Glu	Leu	Pro	Pro	Pro	Pro	Ala	Glu	Pro	Val	Glu	Lys	
1				5					10					15	
Gly	Ala	Ser	Thr	Asp	Ile	Cys	Ala	Phe	Cys	His	Lys	Thr	Val	Phe	
			20						25					30	
Pro	Arg	Glu	Leu	Ala	Val	Glu	Ala	Met	Lys	Arg	Gln	Tyr	His	Ala	
			35						40					45	
Gln	Cys	Phe	Thr	Cys	Arg	Thr	Cys	Arg	Arg	Gln	Leu	Ala	Gly	Gln	
			50						55					60	
Ser	Phe	Tyr	Gln	Lys	Asp	Gly	Arg	Pro	Leu	Cys	Glu	Pro	Cys	Tyr	
			65						70					75	
Gln	Asp	Thr	Leu	Glu	Arg	Cys	Gly	Lys	Cys	Gly	Glu	Val	Val	Arg	
			80						85					90	
Asp	His	Ile	Ile	Arg	Ala	Leu	Gly	Gln	Ala	Phe	His	Pro	Ser	Cys	
			95						100					105	
Phe	Thr	Cys	Val	Thr	Cys	Ala	Arg	Cys	Ile	Gly	Asp	Glu	Ser	Phe	
			110						115					120	
Ala	Leu	Gly	Ser	Gln	Asn	Glu	Val	Tyr	Cys	Leu	Asp	Asp	Phe	Tyr	
			125						130					135	
Arg	Lys	Phe	Ala	Pro	Val	Cys	Ser	Ile	Cys	Glu	Asn	Pro	Ile	Ile	
			140						145					150	
Pro	Arg	Asp	Gly	Lys	Asp	Ala	Phe	Lys	Ile	Glu	Cys	Met	Gly	Arg	
			155						160					165	
Asn	Phe	His	Glu	Asn	Cys	Tyr	Arg	Cys	Glu	Asp	Cys	Arg	Ile	Leu	
			170						175					180	
Leu	Ser	Val	Glu	Pro	Thr	Asp	Gln	Gly	Cys	Tyr	Pro	Leu	Asn	Asn	
			185						190					195	
His	Leu	Phe	Cys	Lys	Pro	Cys	His	Val	Lys	Arg	Ser	Ala	Ala	Gly	
			200						205					210	
Cys	Cys														

<210> 22
 <211> 227
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3092084CD1

<400> 22
 Met Gly Gly Thr Thr Ser Thr Arg Arg Val Thr Phe Glu Ala Asp
 1 5 10 15
 Glu Asn Glu Asn Ile Thr Val Val Lys Gly Ile Arg Leu Ser Glu
 20 25 30
 Asn Val Ile Asp Arg Met Lys Glu Ser Ser Pro Ser Gly Ser Lys
 35 40 45
 Ser Gln Arg Tyr Ser Gly Ala Tyr Gly Ala Ser Val Ser Asp Glu
 50 55 60
 Glu Leu Lys Arg Arg Val Ala Glu Glu Leu Ala Leu Glu Gln Ala
 65 70 75
 Lys Lys Glu Ser Glu Asp Gln Lys Arg Leu Lys Gln Ala Lys Glu
 80 85 90
 Leu Asp Arg Glu Arg Ala Ala Ala Asn Glu Gln Leu Thr Arg Ala
 95 100 105
 Ile Leu Arg Glu Arg Ile Cys Ser Glu Glu Glu Arg Ala Lys Ala
 110 115 120
 Lys His Leu Ala Arg Gln Leu Glu Glu Lys Asp Arg Val Leu Lys
 125 130 135
 Lys Gln Asp Ala Phe Tyr Lys Glu Gln Leu Ala Arg Leu Glu Glu
 140 145 150
 Arg Ser Ser Glu Phe Tyr Arg Val Thr Thr Glu Gln Tyr Gln Lys
 155 160 165
 Ala Ala Glu Glu Val Glu Ala Lys Phe Lys Arg Tyr Glu Ser His
 170 175 180
 Pro Val Cys Ala Asp Leu Gln Ala Lys Ile Leu Gln Cys Tyr Arg
 185 190 195
 Glu Asn Thr His Gln Thr Leu Lys Cys Ser Ala Leu Ala Thr Gln
 200 205 210
 Tyr Met His Cys Val Asn His Ala Lys Gln Ser Met Leu Glu Lys
 215 220 225
 Gly Gly

<210> 23
 <211> 490
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3882482CD1

<400> 23
 Met Asn Leu Ala Glu Ile Cys Asp Asn Ala Lys Lys Gly Arg Glu
 1 5 10 15
 Tyr Ala Leu Leu Gly Asn Tyr Asp Ser Ser Met Val Tyr Tyr Gln
 20 25 30
 Gly Val Met Gln Gln Ile Gln Arg His Cys Gln Ser Val Arg Asp
 35 40 45
 Pro Ala Ile Lys Gly Lys Trp Gln Gln Val Arg Gln Glu Leu Leu
 50 55 60
 Glu Glu Tyr Glu Gln Val Lys Ser Ile Val Ser Thr Leu Glu Ser
 65 70 75
 Phe Lys Ile Asp Lys Pro Pro Asp Phe Pro Val Ser Cys Gln Asp
 80 85 90
 Glu Pro Phe Arg Asp Pro Ala Val Trp Pro Pro Pro Val Pro Ala
 95 100 105

Glu	His	Arg	Ala	Pro	Pro	Gln	Ile	Arg	Arg	Pro	Asn	Arg	Glu	Val
				110					115					120
Arg	Pro	Leu	Arg	Lys	Glu	Met	Ala	Gly	Val	Gly	Ala	Arg	Gly	Pro
				125					130					135
Val	Gly	Arg	Ala	His	Pro	Ile	Ser	Lys	Ser	Glu	Lys	Pro	Ser	Thr
				140					145					150
Ser	Arg	Asp	Lys	Asp	Tyr	Arg	Ala	Arg	Gly	Arg	Asp	Asp	Lys	Gly
				155					160					165
Arg	Lys	Asn	Met	Gln	Asp	Gly	Ala	Ser	Asn	Gly	Glu	Met	Pro	Lys
				170					175					180
Phe	Asp	Gly	Ala	Gly	Tyr	Asp	Lys	Asp	Leu	Val	Glu	Ala	Leu	Glu
				185					190					195
Arg	Asp	Ile	Val	Ser	Arg	Asn	Pro	Ser	Ile	His	Trp	Asp	Asp	Ile
				200					205					210
Ala	Asp	Leu	Glu	Glu	Ala	Lys	Lys	Leu	Leu	Arg	Glu	Ala	Val	Val
				215					220					225
Leu	Pro	Met	Trp	Met	Pro	Asp	Phe	Phe	Lys	Gly	Ile	Arg	Arg	Pro
				230					235					240
Trp	Lys	Gly	Val	Leu	Met	Val	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr
				245					250					255
Met	Leu	Ala	Lys	Ala	Val	Ala	Thr	Glu	Cys	Gly	Thr	Thr	Phe	Phe
				260					265					270
Asn	Val	Ser	Ser	Ser	Thr	Leu	Thr	Ser	Lys	Tyr	Arg	Gly	Glu	Ser
				275					280					285
Glu	Lys	Leu	Val	Arg	Leu	Leu	Phe	Glu	Met	Ala	Arg	Phe	Tyr	Ala
				290					295					300
Pro	Thr	Thr	Ile	Phe	Ile	Asp	Glu	Ile	Asp	Ser	Ile	Cys	Ser	Arg
				305					310					315
Arg	Gly	Thr	Ser	Asp	Glu	His	Glu	Ala	Ser	Arg	Arg	Val	Lys	Ser
				320					325					330
Glu	Leu	Leu	Ile	Gln	Met	Asp	Gly	Val	Gly	Gly	Ala	Leu	Glu	Asn
				335					340					345
Asp	Asp	Pro	Ser	Lys	Met	Val	Met	Val	Leu	Ala	Ala	Thr	Asn	Phe
				350					355					360
Pro	Trp	Asp	Ile	Asp	Glu	Ala	Leu	Arg	Arg	Arg	Leu	Glu	Lys	Arg
				365					370					375
Ile	Tyr	Ile	Pro	Leu	Pro	Thr	Ala	Lys	Gly	Arg	Ala	Glu	Leu	Leu
				380					385					390
Lys	Ile	Asn	Leu	Arg	Glu	Val	Glu	Leu	Asp	Pro	Asp	Ile	Gln	Leu
				395					400					405
Glu	Asp	Ile	Ala	Glu	Lys	Ile	Glu	Gly	Tyr	Ser	Gly	Ala	Asp	Ile
				410					415					420
Thr	Asn	Val	Cys	Arg	Asp	Ala	Ser	Leu	Met	Ala	Met	Arg	Arg	Arg
				425					430					435
Ile	Asn	Gly	Leu	Ser	Pro	Glu	Glu	Ile	Arg	Ala	Leu	Ser	Lys	Glu
				440					445					450
Glu	Leu	Gln	Met	Pro	Val	Thr	Lys	Gly	Asp	Phe	Glu	Leu	Ala	Leu
				455					460					465
Lys	Lys	Ile	Ala	Lys	Ser	Val	Ser	Ala	Ala	Asp	Leu	Glu	Lys	Tyr
				470					475					480
Glu	Lys	Trp	Met	Val	Glu	Phe	Gly	Ser	Ala					
				485					490					

<210> 24

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4933451CD1

<400> 24

Met	Ala	Ala	Arg	Thr	Val	Ile	Ile	Asp	His	Gly	Ser	Gly	Phe	Leu
				5					10					15
Lys	Ala	Gly	Thr	Ala	Gly	Trp	Asn	Glu	Pro	Gln	Met	Val	Phe	Pro
				20					25					30

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Asn Ile Val Asn Tyr Leu Pro Cys Lys Glu Asn Pro Gly Pro Ser
35 40 45
Tyr Ala Arg Lys Arg Val Ser Leu Gly Ile Asp Ile Cys His Pro
50 55 60
Asp Thr Phe Ser Tyr Pro Ile Glu Arg Gly Arg Ile Leu Asn Trp
65 70 75
Glu Gly Val Gln Tyr Leu Trp Ser Phe Val Leu Glu Asn His Arg
80 85 90
Arg Glu Gln Glu Val Pro Pro Val Ile Ile Thr Glu Thr Pro Leu
95 100 105
Arg Glu Pro Ala Asp Arg Lys Lys Met Ser Ser Leu Glu Thr Leu
110 115 120
Gln Gly Thr Val Phe Pro Gly Trp Pro Ile Ile Gly Val
125 130

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<210> 25

<211> 912

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5043904CD1

<400> 25

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Met Ser Asp Ala Gln Gly Ser Tyr Lys Leu Asp Glu Ala Gln Ala
1 5 10 15
Val Leu Arg Glu Thr Lys Ala Ile Lys Lys Ala Ile Thr Cys Gly
20 25 30
Glu Lys Glu Lys Gln Asp Leu Ile Lys Ser Leu Ala Met Leu Lys
35 40 45
Asp Gly Phe Cys Thr Asp Arg Gly Ser His Ser Asp Leu Trp Ser
50 55 60
Ser Ser Ser Ser Leu Glu Ser Ser Ser Phe Pro Leu Pro Lys Gln
65 70 75
Tyr Leu Asp Val Ser Ser Gln Thr Asp Ile Ser Gly Ser Phe Gly
80 85 90
Ile Asn Ser Asn Asn Gln Leu Ala Glu Lys Val Arg Leu Arg Leu
95 100 105
Arg Tyr Glu Glu Ala Lys Arg Arg Ile Ala Asn Leu Lys Ile Gln
110 115 120
Leu Ala Lys Leu Asp Ser Glu Ala Trp Pro Gly Val Leu Asp Ser
125 130 135
Glu Arg Asp Arg Leu Ile Leu Ile Asn Glu Lys Glu Glu Leu Leu
140 145 150
Lys Glu Met Arg Phe Ile Ser Pro Arg Lys Trp Thr Gln Gly Glu
155 160 165
Val Glu Gln Leu Glu Met Ala Arg Lys Arg Leu Glu Lys Asp Leu
170 175 180
Gln Ala Ala Arg Asp Thr Gln Ser Lys Ala Leu Thr Glu Arg Leu
185 190 195
Lys Leu Asn Ser Lys Arg Asn Gln Leu Val Arg Glu Leu Glu Glu
200 205 210
Ala Thr Arg Gln Val Ala Thr Leu His Ser Gln Leu Lys Ser Leu
215 220 225
Ser Ser Ser Met Gln Ser Leu Ser Ser Gly Ser Ser Pro Gly Ser
230 235 240
Leu Thr Ser Ser Arg Gly Ser Leu Val Ala Ser Ser Leu Asp Ser
245 250 255
Ser Thr Ser Ala Ser Phe Thr Asp Leu Tyr Tyr Asp Pro Phe Glu
260 265 270
Gln Leu Asp Ser Glu Leu Gln Ser Lys Val Glu Phe Leu Leu Leu
275 280 285
Glu Gly Ala Thr Gly Phe Arg Pro Ser Gly Cys Ile Thr Thr Ile
290 295 300
His Glu Asp Glu Val Ala Lys Thr Gln Lys Ala Glu Gly Gly Gly
305 310 315

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Arg	Leu	Gln	Ala	Leu	Arg	Ser	Leu	Ser	Gly	Thr	Pro	Lys	Ser	Met
				320					325					330
Thr	Ser	Leu	Ser	Pro	Arg	Ser	Ser	Leu	Ser	Ser	Pro	Ser	Pro	Pro
				335					340					345
Cys	Ser	Pro	Leu	Met	Ala	Asp	Pro	Leu	Leu	Ala	Gly	Asp	Ala	Phe
				350					355					360
Leu	Asn	Ser	Leu	Glu	Phe	Glu	Asp	Pro	Glu	Leu	Ser	Ala	Thr	Leu
				365					370					375
Cys	Glu	Leu	Ser	Leu	Gly	Asn	Ser	Ala	Gln	Glu	Arg	Tyr	Arg	Leu
				380					385					390
Glu	Glu	Pro	Gly	Thr	Glu	Gly	Lys	Gln	Leu	Gly	Gln	Ala	Val	Asn
				395					400					405
Thr	Ala	Gln	Gly	Cys	Gly	Leu	Lys	Val	Ala	Cys	Val	Ser	Ala	Ala
				410					415					420
Val	Ser	Asp	Glu	Ser	Val	Ala	Gly	Asp	Ser	Gly	Val	Tyr	Glu	Ala
				425					430					435
Ser	Val	Gln	Arg	Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Phe	Asp	Ser
				440					445					450
Asp	Glu	Ser	Glu	Ala	Val	Gly	Ala	Thr	Arg	Ile	Gln	Ile	Ala	Leu
				455					460					465
Lys	Tyr	Asp	Glu	Lys	Asn	Lys	Gln	Phe	Ala	Ile	Leu	Ile	Ile	Gln
				470					475					480
Leu	Ser	Asn	Leu	Ser	Ala	Leu	Leu	Gln	Gln	Gln	Asp	Gln	Lys	Val
				485					490					495
Asn	Ile	Arg	Val	Ala	Val	Leu	Pro	Cys	Ser	Glu	Ser	Thr	Thr	Cys
				500					505					510
Leu	Phe	Arg	Thr	Arg	Pro	Leu	Asp	Ala	Ser	Asp	Thr	Leu	Val	Phe
				515					520					525
Asn	Glu	Val	Phe	Trp	Val	Ser	Met	Ser	Tyr	Pro	Ala	Leu	His	Gln
				530					535					540
Lys	Thr	Leu	Arg	Val	Asp	Val	Cys	Thr	Thr	Asp	Arg	Ser	His	Leu
				545					550					555
Glu	Glu	Cys	Leu	Gly	Gly	Ala	Gln	Ile	Ser	Leu	Ala	Glu	Val	Cys
				560					565					570
Arg	Ser	Gly	Glu	Arg	Ser	Thr	Arg	Trp	Tyr	Asn	Leu	Leu	Ser	Tyr
				575					580					585
Lys	Tyr	Leu	Lys	Lys	Gln	Ser	Arg	Glu	Leu	Lys	Pro	Val	Gly	Val
				590					595					600
Met	Ala	Pro	Ala	Ser	Gly	Pro	Ala	Ser	Thr	Asp	Ala	Val	Ser	Ala
				605					610					615
Leu	Leu	Glu	Gln	Thr	Ala	Val	Glu	Leu	Glu	Lys	Arg	Gln	Glu	Gly
				620					625					630
Arg	Ser	Ser	Thr	Gln	Thr	Leu	Glu	Asp	Ser	Trp	Arg	Tyr	Glu	Glu
				635					640					645
Thr	Ser	Glu	Asn	Glu	Ala	Val	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val
				650					655					660
Glu	Glu	Glu	Glu	Gly	Glu	Glu	Asp	Val	Phe	Thr	Glu	Lys	Ala	Ser
				665					670					675
Pro	Asp	Met	Asp	Gly	Tyr	Pro	Ala	Leu	Lys	Val	Asp	Lys	Glu	Thr
				680					685					690
Asn	Thr	Glu	Thr	Pro	Ala	Pro	Ser	Pro	Thr	Val	Val	Arg	Pro	Lys
				695					700					705
Asp	Arg	Arg	Val	Gly	Thr	Pro	Ser	Gln	Gly	Pro	Phe	Leu	Arg	Gly
				710					715					720
Ser	Thr	Ile	Ile	Arg	Ser	Lys	Thr	Phe	Ser	Pro	Gly	Pro	Gln	Ser
				725					730					735
Gln	Tyr	Val	Cys	Arg	Leu	Asn	Arg	Ser	Asp	Ser	Asp	Ser	Ser	Thr
				740					745					750
Leu	Ser	Lys	Lys	Pro	Pro	Phe	Val	Arg	Asn	Ser	Leu	Glu	Arg	Arg
				755					760					765
Ser	Val	Arg	Met	Lys	Arg	Pro	Ser	Ser	Val	Lys	Ser	Leu	Arg	Ser
				770					775					780
Glu	Arg	Leu	Ile	Arg	Thr	Ser	Leu	Asp	Leu	Glu	Leu	Asp	Leu	Gln
				785					790					795
Ala	Thr	Arg	Thr	Trp	His	Ser	Gln	Leu	Thr	Gln	Glu	Ile	Ser	Val
				800					805					810
Leu	Lys	Glu	Leu	Lys	Glu	Gln	Leu	Glu	Gln	Ala	Lys	Ser	His	Gly

	815		820		825
Glu Lys Glu Leu	Pro Gln Trp Leu Arg	Glu Asp Glu Arg Phe	Arg		
	830		835		840
Leu Leu Leu Arg	Met Leu Glu Lys Arg	Gln Met Asp Arg Ala	Glu		
	845		850		855
His Lys Gly Glu	Leu Gln Thr Asp Lys	Met Met Arg Ala Ala	Ala		
	860		865		870
Lys Asp Val His	Arg Leu Arg Gly Gln	Ser Cys Lys Glu Pro	Pro		
	875		880		885
Glu Val Gln Ser	Phe Arg Glu Lys Met	Ala Phe Phe Thr Arg	Pro		
	890		895		900
Arg Met Asn Ile	Pro Ala Leu Ser Ala	Asp Asp Val			
	905		910		

<210> 26

<211> 1076

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5202390CD1

<400> 26

Met Lys Gln Tyr	Ala Ser Pro Met Pro Thr	Gln Thr Asp Val Lys	
1	5	10	15
Leu Lys Phe Lys	Pro Leu Ser Lys Lys Val	Val Ser Ala Ala Leu	
	20	25	30
Gln Phe Ser Leu	Ser Cys Ile Phe Leu Arg	Glu Gly Lys Ala Thr	
	35	40	45
Asp Glu Asp Met	Gln Ser Leu Ala Ser Leu	Met Ser Met Lys Gln	
	50	55	60
Ala Asp Ile Gly	Asn Leu Asp Asp Phe Glu	Glu Asp Asn Glu Asp	
	65	70	75
Asp Asp Glu Asn	Arg Val Asn Gln Glu Glu	Lys Ala Ala Lys Ile	
	80	85	90
Thr Glu Leu Ile	Asn Lys Leu Asn Phe Leu	Asp Glu Ala Glu Lys	
	95	100	105
Asp Leu Ala Thr	Val Asn Ser Asn Pro Phe	Asp Asp Pro Asp Ala	
	110	115	120
Ala Glu Leu Asn	Pro Phe Gly Asp Pro Asp	Ser Glu Glu Pro Ile	
	125	130	135
Thr Glu Thr Ala	Ser Pro Arg Lys Thr Glu	Asp Ser Phe Tyr Asn	
	140	145	150
Asn Ser Tyr Asn	Pro Phe Lys Glu Val Gln	Thr Pro Gln Tyr Leu	
	155	160	165
Asn Pro Phe Asp	Glu Pro Glu Ala Phe Val	Thr Ile Lys Asp Ser	
	170	175	180
Pro Pro Gln Ser	Thr Lys Arg Lys Asn Ile	Arg Pro Val Asp Met	
	185	190	195
Ser Lys Tyr Leu	Tyr Ala Asp Ser Ser Lys	Thr Glu Glu Glu Glu	
	200	205	210
Leu Asp Glu Ser	Asn Pro Phe Tyr Glu Pro	Lys Ser Thr Pro Pro	
	215	220	225
Pro Asn Asn Leu	Val Asn Pro Val Gln Glu	Leu Glu Thr Glu Arg	
	230	235	240
Arg Val Lys Arg	Lys Ala Pro Ala Pro Pro	Val Leu Ser Pro Lys	
	245	250	255
Thr Gly Val Leu	Asn Glu Asn Thr Val Ser	Ala Gly Lys Asp Leu	
	260	265	270
Ser Thr Ser Pro	Lys Pro Ser Pro Ile Pro	Ser Pro Val Leu Gly	
	275	280	285
Arg Lys Pro Asn	Ala Ser Gln Ser Leu Leu	Val Trp Cys Lys Glu	
	290	295	300
Val Thr Lys Asn	Tyr Arg Gly Val Lys Ile	Thr Asn Phe Thr Thr	
	305	310	315
Ser Trp Arg Asn	Gly Leu Ser Phe Cys Ala	Ile Leu His His Phe	

Arg	Pro	Asp	Leu	320	Ile	Asp	Tyr	Lys	Ser	Leu	Asn	Pro	Gln	Asp	Ile	330
				335												345
Lys	Glu	Asn	Asn	350	Lys	Lys	Ala	Tyr	Asp	Gly	Phe	Ala	Ser	Ile	Gly	360
Ile	Ser	Arg	Leu	365	Leu	Glu	Pro	Ser	Asp	Met	Val	Leu	Leu	Ala	Ile	375
Pro	Asp	Lys	Leu	380	Thr	Val	Met	Thr	Tyr	Leu	Tyr	Gln	Ile	Arg	Ala	390
His	Phe	Ser	Gly	395	Gln	Glu	Leu	Asn	Val	Val	Gln	Ile	Glu	Glu	Asn	405
Ser	Ser	Lys	Ser	410	Thr	Tyr	Lys	Val	Gly	Asn	Tyr	Glu	Thr	Asp	Thr	420
Asn	Ser	Ser	Val	425	Asp	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Leu	Ser	Asp	435
Leu	Lys	Arg	Glu	440	Pro	Glu	Leu	Gln	Gln	Pro	Ile	Ser	Gly	Ala	Val	450
Asp	Phe	Leu	Ser	455	Gln	Asp	Asp	Ser	Val	Phe	Val	Asn	Asp	Ser	Gly	465
Val	Gly	Glu	Ser	470	Glu	Ser	Glu	His	Gln	Thr	Pro	Asp	Asp	His	Leu	480
Ser	Pro	Ser	Thr	485	Ala	Ser	Pro	Tyr	Cys	Arg	Arg	Thr	Lys	Ser	Asp	495
Thr	Glu	Pro	Gln	500	Lys	Ser	Gln	Gln	Ser	Ser	Gly	Arg	Thr	Ser	Gly	510
Ser	Asp	Asp	Pro	515	Gly	Ile	Cys	Ser	Asn	Thr	Asp	Ser	Thr	Gln	Ala	525
Gln	Val	Leu	Leu	530	Gly	Lys	Lys	Arg	Leu	Leu	Lys	Ala	Glu	Thr	Leu	540
Glu	Leu	Ser	Asp	545	Leu	Tyr	Val	Ser	Asp	Lys	Lys	Lys	Asp	Met	Ser	555
Pro	Pro	Phe	Ile	560	Cys	Glu	Glu	Thr	Asp	Glu	Gln	Lys	Leu	Gln	Thr	570
Leu	Asp	Ile	Gly	575	Ser	Asn	Leu	Glu	Lys	Glu	Lys	Leu	Glu	Asn	Ser	585
Arg	Ser	Leu	Glu	590	Cys	Arg	Ser	Asp	Pro	Glu	Ser	Pro	Ile	Lys	Lys	600
Thr	Ser	Leu	Ser	605	Pro	Thr	Ser	Lys	Leu	Gly	Tyr	Ser	Tyr	Ser	Arg	615
Asp	Leu	Asp	Leu	620	Ala	Lys	Lys	Lys	His	Ala	Ser	Leu	Arg	Gln	Thr	630
Glu	Ser	Asp	Pro	635	Asp	Ala	Asp	Arg	Thr	Thr	Leu	Asn	His	Ala	Asp	645
His	Ser	Ser	Lys	650	Ile	Val	Gln	His	Arg	Leu	Leu	Ser	Arg	Gln	Glu	660
Glu	Leu	Lys	Glu	665	Arg	Ala	Arg	Val	Leu	Leu	Glu	Gln	Ala	Arg	Arg	675
Asp	Ala	Ala	Leu	680	Lys	Ala	Gly	Asn	Lys	His	Asn	Thr	Asn	Thr	Ala	690
Thr	Pro	Phe	Cys	695	Asn	Arg	Gln	Leu	Ser	Asp	Gln	Gln	Asp	Glu	Glu	705
Arg	Arg	Arg	Gln	710	Leu	Arg	Glu	Arg	Ala	Arg	Gln	Leu	Ile	Ala	Glu	720
Ala	Arg	Ser	Gly	725	Val	Lys	Met	Ser	Glu	Leu	Pro	Ser	Tyr	Gly	Glu	735
Met	Ala	Ala	Glu	740	Lys	Leu	Lys	Glu	Arg	Ser	Lys	Ala	Ser	Gly	Asp	750
Glu	Asn	Asp	Asn	755	Ile	Glu	Ile	Asp	Thr	Asn	Glu	Glu	Ile	Pro	Glu	765
Gly	Phe	Val	Val	770	Gly	Gly	Gly	Asp	Glu	Leu	Thr	Asn	Leu	Glu	Asn	780
Asp	Leu	Asp	Thr	785	Pro	Glu	Gln	Asn	Ser	Lys	Leu	Val	Asp	Leu	Lys	795
Leu	Lys	Lys	Leu	800	Leu	Glu	Val	Gln	Pro	Gln	Val	Ala	Asn	Ser	Pro	810
Ser	Ser	Ala	Ala	815	Gln	Lys	Ala	Val	Thr	Glu	Ser	Ser	Glu	Gln	Asp	825

Met Lys Ser Gly	Thr	Glu Asp Leu Arg	Thr	Glu Arg Leu Gln	Lys	
	830		835		840	
Thr Thr Glu Arg	Phe	Arg Asn Pro Val	Val	Phe Ser Lys Asp	Ser	
	845		850		855	
Thr Val Arg Lys	Thr	Gln Leu Gln Ser	Phe	Ser Gln Tyr Ile	Glu	
	860		865		870	
Asn Arg Pro Glu	Met	Lys Arg Gln Arg	Ser	Ile Gln Glu Asp	Thr	
	875		880		885	
Lys Lys Gly Asn	Glu	Glu Lys Ala Ala	Ile	Thr Glu Thr Gln	Arg	
	890		895		900	
Lys Pro Ser Glu	Asp	Glu Val Leu Asn	Lys	Gly Phe Lys Asp	Thr	
	905		910		915	
Ser Gln Tyr Val	Val	Gly Glu Leu Ala	Ala	Leu Glu Asn Glu	Gln	
	920		925		930	
Lys Gln Ile Asp	Thr	Arg Ala Ala Leu	Val	Glu Lys Arg Leu	Arg	
	935		940		945	
Tyr Leu Met Asp	Thr	Gly Arg Asn Thr	Glu	Glu Glu Glu Ala	Met	
	950		955		960	
Met Gln Glu Trp	Phe	Met Leu Val Asn	Lys	Lys Asn Ala Leu	Ile	
	965		970		975	
Arg Arg Met Asn	Gln	Leu Ser Leu Leu	Glu	Lys Glu His Asp	Leu	
	980		985		990	
Glu Arg Arg Tyr	Glu	Leu Leu Asn Arg	Glu	Leu Arg Ala Met	Leu	
	995		1000		1005	
Ala Ile Glu Asp	Trp	Gln Lys Thr Glu	Ala	Gln Lys Arg Arg	Glu	
	1010		1015		1020	
Gln Leu Leu Leu	Asp	Glu Leu Val Ala	Leu	Val Asn Lys Arg	Asp	
	1025		1030		1035	
Ala Leu Val Arg	Asp	Leu Asp Ala Gln	Glu	Lys Gln Ala Glu	Glu	
	1040		1045		1050	
Glu Asp Glu His	Leu	Glu Arg Thr Leu	Glu	Gln Asn Lys Gly	Lys	
	1055		1060		1065	
Met Ala Lys Lys	Glu	Glu Lys Cys Val	Leu	Gln		
	1070		1075			

<210> 27

<211> 542

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5526375CD1

<400> 27

Met Glu Glu Arg Gly	Ser Pro Asp Gly Asp	Leu Ala Arg Ser Leu
1	5	10
Glu Gln Gly Pro Glu	Gly Pro Glu Thr	Pro Ile Gln Val Val Leu
	20	25
Arg Val Arg Pro Met	Ser Ala Ala Glu Leu	Arg Arg Gly Gln Gln
	35	40
Ser Val Leu His Cys	Ser Gly Thr Arg Thr	Leu Gln Val Ser Pro
	50	55
Pro Gly Gly Gly Pro	Glu Val Ala Phe Arg	Phe Gly Ala Val Leu
	65	70
Asp Ala Ala Arg Thr	Gln Glu Asp Val Phe	Arg Ala Cys Gly Val
	80	85
Arg Arg Leu Gly Glu	Leu Ala Leu Arg Gly	Phe Ser Cys Thr Val
	95	100
Phe Thr Phe Gly Gln	Thr Gly Ser Gly Lys	Thr Tyr Thr Leu Thr
	110	115
Gly Pro Pro Pro Gln	Gly Glu Gly Val Pro	Val Pro Pro Ser Leu
	125	130
Ala Gly Ile Met Gln	Arg Thr Phe Ala Trp	Leu Leu Asp Arg Val
	140	145
Gln His Leu Gly Ala	Pro Val Thr Leu Arg	Ala Ser Tyr Leu Glu
	155	160

Ile Tyr Asn Gly	Gln Val Arg Asp Leu	Leu Ser Leu Gly Ser	Pro
	170	175	180
Arg Pro Leu Pro	Val Arg Trp Asn Lys	Thr Arg Gly Phe Tyr	Val
	185	190	195
Glu Gln Leu Arg	Val Val Glu Phe Gly	Ser Leu Glu Ala Leu	Met
	200	205	210
Glu Leu Leu Gln	Thr Gly Leu Ser Arg	Arg Arg Asn Ser Ala	His
	215	220	225
Thr Leu Asn Gln	Ala Ser Ser Arg Ser	His Ala Leu Leu Thr	Leu
	230	235	240
Tyr Ile Ser Arg	Gln Thr Ala Gln Gln	Met Pro Ser Val Asp	Pro
	245	250	255
Gly Glu Pro Pro	Val Gly Gly Lys Leu	Cys Phe Val Asp Leu	Ala
	260	265	270
Gly Ser Glu Lys	Val Ala Ala Thr Gly	Ser Arg Gly Glu Leu	Met
	275	280	285
Leu Glu Ala Asn	Ser Ile Asn Arg Ser	Leu Leu Ala Leu Gly	His
	290	295	300
Cys Ile Ser Leu	Leu Asp Pro Gln	Arg Lys Gln Ser His	Ile
	305	310	315
Pro Phe Arg Asp	Ser Lys Leu Thr Lys	Leu Leu Ala Asp Ser	Leu
	320	325	330
Gly Gly Arg Gly	Val Thr Leu Met Val	Ala Cys Val Ser Pro	Ser
	335	340	345
Ala Gln Cys Leu	Pro Glu Thr Leu Ser	Thr Leu Arg Tyr Ala	Ser
	350	355	360
Arg Ala Gln Arg	Val Thr Thr Arg Pro	Gln Ala Pro Lys Ser	Pro
	365	370	375
Val Ala Lys Gln	Pro Gln Arg Leu Glu	Thr Glu Met Leu Gln	Leu
	380	385	390
Gln Glu Glu Asn	Arg Arg Leu Gln Phe	Gln Leu Asp Gln Met	Asp
	395	400	405
Cys Lys Ala Ser	Gly Leu Ser Gly Ala	Arg Val Ala Trp Ala	Gln
	410	415	420
Arg Asn Leu Tyr	Gly Met Leu Gln Glu	Phe Met Leu Glu Asn	Glu
	425	430	435
Arg Leu Arg Lys	Glu Lys Ser Gln Leu	Gln Asn Ser Arg Glu	Leu
	440	445	450
Ala Gln Asn Glu	Gln Arg Ile Leu Ala	Gln Gln Val His Ala	Leu
	455	460	465
Glu Arg Arg Leu	Leu Ser Ala Cys Tyr	His His Gln Gln Gly	Pro
	470	475	480
Gly Leu Thr Pro	Pro Cys Pro Cys Leu	Met Ala Pro Ala Pro	Pro
	485	490	495
Cys His Ala Leu	Pro Pro Leu Tyr Ser	Cys Pro Cys Cys His	Ile
	500	505	510
Cys Pro Leu Cys	Arg Val Pro Leu Ala	His Trp Gly Cys Leu	Pro
	515	520	525
Gly Glu His His	Leu Pro Gln Pro Leu	Phe Trp Ala Leu Arg	Ser
	530	535	540
Gln Lys			

<210> 28

<211> 351

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5677408CD1

<400> 28

Met Pro Ser Glu Thr	Leu Trp Glu Ile Ala	Lys Ala Glu Val Glu
1	5	10
Lys Arg Gly Ile Asn	Gly Ser Glu Gly Asp	Gly Ala Glu Ile Ala
	20	25
		30

Glu Lys Phe Val Phe Phe Ile Gly Ser Lys Asn Gly Gly Lys Thr
 35 40 45
 Thr Ile Ile Leu Arg Cys Leu Asp Arg Asp Glu Pro Pro Lys Pro
 50 55 60
 Thr Leu Ala Leu Glu Tyr Thr Tyr Gly Arg Arg Ala Lys Gly His
 65 70 75
 Asn Thr Pro Lys Asp Ile Ala His Phe Trp Glu Leu Gly Gly Gly
 80 85 90
 Thr Ser Leu Leu Asp Leu Ile Ser Ile Pro Ile Thr Gly Asp Thr
 95 100 105
 Leu Arg Thr Phe Ser Leu Val Leu Val Leu Asp Leu Ser Lys Pro
 110 115 120
 Asn Asp Leu Trp Pro Thr Met Glu Asn Leu Leu Gln Ala Thr Lys
 125 130 135
 Ser His Val Asp Lys Val Ile Met Lys Leu Gly Lys Thr Asn Ala
 140 145 150
 Lys Ala Val Ser Glu Met Arg Gln Lys Ile Trp Asn Asn Met Pro
 155 160 165
 Lys Asp His Pro Asp His Glu Leu Ile Asp Pro Phe Pro Val Pro
 170 175 180
 Leu Val Ile Ile Gly Ser Lys Tyr Asp Val Phe Gln Asp Phe Glu
 185 190 195
 Ser Glu Lys Arg Lys Val Ile Cys Lys Thr Leu Arg Phe Val Ala
 200 205 210
 His Tyr Tyr Gly Ala Ser Leu Met Phe Thr Ser Lys Ser Glu Ala
 215 220 225
 Leu Leu Leu Lys Ile Arg Gly Val Ile Asn Gln Leu Ala Phe Gly
 230 235 240
 Ile Asp Lys Ser Lys Ser Ile Cys Val Asp Gln Asn Lys Pro Leu
 245 250 255
 Phe Ile Thr Ala Gly Leu Asp Ser Phe Gly Gln Ile Gly Ser Pro
 260 265 270
 Pro Val Pro Glu Asn Asp Ile Gly Lys Leu His Ala His Ser Pro
 275 280 285
 Met Glu Leu Trp Lys Lys Val Tyr Glu Lys Leu Phe Pro Pro Lys
 290 295 300
 Ser Ile Asn Thr Leu Lys Asp Ile Lys Asp Pro Ala Arg Asp Pro
 305 310 315
 Gln Tyr Ala Glu Asn Glu Val Asp Glu Met Arg Ile Gln Lys Asp
 320 325 330
 Leu Glu Leu Glu Gln Tyr Lys Arg Ser Ser Ser Lys Ser Trp Lys
 335 340 345
 Gln Ile Glu Leu Asp Ser
 350

<210> 29

<211> 856

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5982278CD1

<400> 29

Met Lys Ser Ala Arg Ala Lys Thr Pro Arg Lys Pro Thr Val Lys
 1 5 10 15
 Lys Gly Ser Gln Thr Asn Leu Lys Asp Pro Val Gly Val Tyr Cys
 20 25 30
 Arg Val Arg Pro Leu Gly Phe Pro Asp Gln Glu Cys Cys Ile Glu
 35 40 45
 Val Ile Asn Asn Thr Thr Val Gln Leu His Thr Pro Glu Gly Tyr
 50 55 60
 Arg Leu Asn Arg Asn Gly Asp Tyr Lys Glu Thr Gln Tyr Ser Phe
 65 70 75
 Lys Gln Val Phe Gly Thr His Thr Thr Gln Lys Glu Leu Phe Asp
 80 85 90

Val	Val	Ala	Asn	Pro	Leu	Val	Asn	Asp	Leu	Ile	His	Gly	Lys	Asn
				95					100					105
Gly	Leu	Leu	Phe	Thr	Tyr	Gly	Val	Thr	Gly	Ser	Gly	Lys	Thr	His
				110					115					120
Thr	Met	Thr	Gly	Ser	Pro	Gly	Glu	Gly	Gly	Leu	Leu	Pro	Arg	Cys
				125					130					135
Leu	Asp	Met	Ile	Phe	Asn	Ser	Ile	Gly	Ser	Phe	Gln	Ala	Lys	Arg
				140					145					150
Tyr	Val	Phe	Lys	Ser	Asn	Asp	Arg	Asn	Ser	Met	Asp	Ile	Gln	Cys
				155					160					165
Glu	Val	Asp	Ala	Leu	Leu	Glu	Arg	Gln	Lys	Arg	Glu	Ala	Met	Pro
				170					175					180
Asn	Pro	Lys	Thr	Ser	Ser	Ser	Lys	Arg	Gln	Val	Asp	Pro	Glu	Phe
				185					190					195
Ala	Asp	Met	Ile	Thr	Val	Gln	Glu	Phe	Cys	Lys	Ala	Glu	Glu	Val
				200					205					210
Asp	Glu	Asp	Ser	Val	Tyr	Gly	Val	Phe	Val	Ser	Tyr	Ile	Glu	Ile
				215					220					225
Tyr	Asn	Asn	Tyr	Ile	Tyr	Asp	Leu	Leu	Glu	Glu	Val	Pro	Phe	Asp
				230					235					240
Pro	Ile	Asn	Pro	Asn	Leu	His	Asn	Leu	Asn	Cys	Phe	Val	Lys	Ile
				245					250					255
Lys	Asn	His	Asn	Met	Tyr	Val	Ala	Gly	Cys	Thr	Glu	Val	Glu	Val
				260					265					270
Lys	Ser	Thr	Glu	Glu	Ala	Phe	Glu	Val	Phe	Trp	Arg	Gly	Gln	Lys
				275					280					285
Lys	Arg	Arg	Ile	Ala	Asn	Thr	His	Leu	Asn	Arg	Glu	Ser	Ser	Arg
				290					295					300
Ser	His	Ser	Val	Phe	Asn	Ile	Lys	Leu	Val	Gln	Ala	Pro	Leu	Asp
				305					310					315
Ala	Asp	Gly	Asp	Asn	Val	Leu	Gln	Glu	Lys	Glu	Gln	Ile	Thr	Ile
				320					325					330
Ser	Gln	Leu	Ser	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Thr	Asn
				335					340					345
Arg	Thr	Arg	Ala	Glu	Gly	Asn	Arg	Leu	Arg	Glu	Ala	Gly	Asn	Ile
				350					355					360
Asn	Gln	Ser	Leu	Met	Thr	Leu	Arg	Thr	Cys	Met	Asp	Val	Leu	Arg
				365					370					375
Glu	Asn	Gln	Met	Tyr	Gly	Thr	Asn	Lys	Met	Val	Pro	Tyr	Arg	Asp
				380					385					390
Ser	Lys	Leu	Thr	His	Leu	Phe	Lys	Asn	Tyr	Phe	Asp	Gly	Glu	Gly
				395					400					405
Lys	Val	Arg	Met	Ile	Val	Cys	Val	Asn	Pro	Lys	Ala	Glu	Asp	Tyr
				410					415					420
Glu	Glu	Asn	Leu	Gln	Val	Met	Arg	Phe	Ala	Glu	Val	Thr	Gln	Glu
				425					430					435
Val	Glu	Val	Ala	Arg	Pro	Val	Asp	Lys	Ala	Ile	Cys	Gly	Leu	Thr
				440					445					450
Pro	Gly	Arg	Arg	Tyr	Arg	Asn	Gln	Pro	Arg	Gly	Pro	Val	Gly	Asn
				455					460					465
Glu	Pro	Leu	Val	Thr	Asp	Val	Val	Leu	Gln	Ser	Phe	Pro	Pro	Leu
				470					475					480
Pro	Ser	Cys	Glu	Ile	Leu	Asp	Ile	Asn	Asp	Glu	Gln	Thr	Leu	Pro
				485					490					495
Arg	Leu	Ile	Glu	Ala	Leu	Glu	Lys	Arg	His	Asn	Leu	Arg	Gln	Met
				500					505					510
Met	Ile	Asp	Glu	Phe	Asn	Lys	Gln	Ser	Asn	Ala	Phe	Lys	Ala	Leu
				515					520					525
Leu	Gln	Glu	Phe	Asp	Asn	Ala	Val	Leu	Ser	Lys	Glu	Asn	His	Met
				530					535					540
Gln	Gly	Lys	Leu	Asn	Glu	Lys	Glu	Lys	Met	Ile	Ser	Gly	Gln	Lys
				545					550					555
Leu	Glu	Ile	Glu	Arg	Leu	Glu	Lys	Lys	Asn	Lys	Thr	Leu	Glu	Tyr
				560					565					570
Lys	Ile	Glu	Ile	Leu	Glu	Lys	Thr	Thr	Thr	Ile	Tyr	Glu	Glu	Asp
				575					580					585
Lys	Arg	Asn	Leu	Gln	Gln	Glu	Leu	Glu	Thr	Gln	Asn	Gln	Lys	Leu

Gln Arg Gln Phe	590	Ser Asp Lys Arg Arg	595	Leu Glu Ala Arg Leu	600
	605		610		615
Gly Met Val Thr	620	Glu Thr Thr Met Lys	625	Trp Glu Lys Glu Cys	630
	635		640		645
Arg Arg Val Ala	650	Ala Lys Gln Leu Glu	655	Met Gln Asn Lys Leu	660
	665		670		675
Val Lys Asp Glu	680	Lys Leu Lys Gln Leu	685	Lys Ala Ile Val Thr	690
	695		700		705
Pro Lys Thr Glu	710	Lys Pro Glu Arg Pro	715	Ser Arg Glu Arg Asp	720
	725		730		735
Glu Lys Val Thr	740	Gln Arg Ser Val Ser	745	Pro Ser Pro Val Pro	750
	755		760		765
Leu Phe Gln Pro	770	Asp Gln Asn Ala Pro	775	Pro Ile Arg Leu Arg	780
	785		790		795
Arg Arg Ser Arg	800	Ser Ala Gly Asp Arg	805	Trp Val Asp His Lys	810
	815		820		825
Ala Ser Asn Met	830	Gln Thr Glu Thr Val	835	Met Gln Pro His Val	840
	845		850		855
His Ala Ile Thr		Val Ser Val Ala Asn		Glu Lys Ala Leu Ala	
Cys Glu Lys Tyr		Met Leu Thr His Gln		Glu Leu Ala Ser Asp	
Glu Ile Glu Thr		Lys Leu Ile Lys Gly		Asp Ile Tyr Lys Thr	
Gly Gly Gly Gln		Ser Val Gln Phe Thr		Asp Ile Glu Thr Leu	
Gln Glu Ser Pro		Asn Gly Ser Arg Lys		Arg Arg Ser Ser Thr	
Ala Pro Ala Gln		Pro Asp Gly Ala Glu		Ser Glu Trp Thr Asp	
Glu Thr Arg Cys		Ser Val Ala Val Glu		Met Arg Ala Gly Ser	
Leu Gly Pro Gly		Tyr Gln His His Ala		Gln Pro Lys Arg Lys	
Pro					

<210> 30

<211> 1056

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 6437362CD1

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Pro Glu Pro Pro Pro	25	Glu Pro Ala Phe Ser	35	Glu Ala Gln Lys Trp	45
	40		50		60
Ile Glu Gln Val Thr	55	Gly Arg Ser Phe Gly	65	Asp Lys Asp Phe Arg	75
	70		80		90
Thr Gly Leu Glu Asn	85	Gly Ile Leu Leu Cys	95	Glu Leu Leu Asn Ala	105
	100		110		120
Ile Lys Pro Gly Leu	115	Val Lys Lys Ile Asn	125	Arg Leu Pro Thr Pro	135
	130		140		150
Ile Ala Gly Leu Asp	145	Asn Ile Ile Leu Phe	155	Leu Arg Gly Cys Lys	165
	160		170		180
Glu Leu Gly Leu Lys	185	Glu Ser Gln Leu Phe	195	Asp Pro Ser Asp Leu	205
	210		220		230
Gln Asp Thr Ser Asn	235	Arg Val Thr Val Lys	245	Ser Leu Asp Tyr Ser	255
	260		270		280
Arg Lys Leu Lys Asn	285	Val Leu Val Thr Ile	295	Tyr Trp Leu Gly Lys	305
	310		320		330
Ala Ala Asn Ser Cys	335	Thr Ser Tyr Ser Gly	345	Thr Thr Leu Asn Leu	355

	140		145		150
Lys Glu Phe Glu Gly	Leu Leu Ala Gln Met	Arg Lys Asp Thr	Asp		
	155		160		165
Asp Ile Glu Ser Pro	Lys Arg Ser Ile Arg	Asp Ser Gly Tyr	Ile		
	170		175		180
Asp Cys Trp Asp Ser	Glu Arg Ser Asp Ser	Leu Ser Pro Pro	Arg		
	185		190		195
His Gly Arg Asp Asp	Ser Phe Asp Ser Leu	Asp Ser Phe Gly	Ser		
	200		205		210
Arg Ser Arg Gln Thr	Pro Ser Pro Asp Val	Val Leu Arg Gly	Ser		
	215		220		225
Ser Asp Gly Arg Gly	Ser Asp Ser Glu Ser	Asp Leu Pro His	Arg		
	230		235		240
Lys Leu Pro Asp Val	Lys Lys Asp Asp Met	Ser Ala Arg Arg	Thr		
	245		250		255
Ser His Gly Glu Pro	Lys Ser Ala Val Pro	Phe Asn Gln Tyr	Leu		
	260		265		270
Pro Asn Lys Ser Asn	Gln Thr Ala Tyr Val	Pro Ala Pro Leu	Arg		
	275		280		285
Lys Lys Lys Ala Glu	Arg Glu Glu Tyr Arg	Lys Ser Trp Ser	Thr		
	290		295		300
Ala Thr Ser Pro Leu	Gly Gly Glu Arg Pro	Phe Arg Tyr Gly	Pro		
	305		310		315
Arg Thr Pro Val Ser	Asp Asp Ala Glu Ser	Thr Ser Met Phe	Asp		
	320		325		330
Met Arg Cys Glu Glu	Ala Ala Val Gln	Pro His Ser Arg	Ala		
	335		340		345
Arg Gln Glu Gln Leu	Gln Leu Ile Asn Asn	Gln Leu Arg Glu	Glu		
	350		355		360
Asp Asp Lys Trp Gln	Asp Asp Leu Ala Arg	Trp Lys Ser Arg	Arg		
	365		370		375
Arg Ser Val Ser Gln	Asp Leu Ile Lys Lys	Glu Glu Glu Arg	Lys		
	380		385		390
Lys Met Glu Lys Leu	Leu Ala Gly Glu Asp	Gly Thr Ser Glu	Arg		
	395		400		405
Arg Lys Ser Ile Lys	Thr Tyr Arg Glu Ile	Val Gln Glu Lys	Glu		
	410		415		420
Arg Arg Glu Arg Glu	Leu His Glu Ala Tyr	Lys Asn Ala Arg	Ser		
	425		430		435
Gln Glu Glu Ala Glu	Gly Ile Leu Gln Gln	Tyr Ile Glu Arg	Phe		
	440		445		450
Thr Ile Ser Glu Ala	Val Leu Glu Arg Leu	Glu Met Pro Lys	Ile		
	455		460		465
Leu Glu Arg Ser His	Ser Thr Glu Pro Asn	Leu Ser Ser Phe	Leu		
	470		475		480
Asn Asp Pro Asn Pro	Met Lys Tyr Leu Arg	Gln Gln Ser Leu	Pro		
	485		490		495
Pro Pro Lys Phe Thr	Ala Thr Val Glu Thr	Thr Ile Ala Arg	Ala		
	500		505		510
Ser Val Leu Asp Thr	Ser Met Ser Ala Gly	Ser Gly Ser Pro	Ser		
	515		520		525
Lys Thr Val Thr Pro	Lys Ala Val Pro Met	Leu Thr Pro Lys	Pro		
	530		535		540
Tyr Ser Gln Pro Lys	Asn Ser Gln Asp Val	Leu Lys Thr Phe	Lys		
	545		550		555
Val Asp Gly Lys Val	Ser Val Asn Gly Glu	Thr Val His Arg	Glu		
	560		565		570
Glu Glu Lys Glu Arg	Glu Cys Pro Thr Val	Ala Pro Ala His	Ser		
	575		580		585
Leu Thr Lys Ser Gln	Met Phe Glu Gly Val	Ala Arg Val His	Gly		
	590		595		600
Ser Pro Leu Glu Leu	Lys Gln Asp Asn Gly	Ser Ile Glu Ile	Asn		
	605		610		615
Ile Lys Lys Pro Asn	Ser Val Pro Gln Glu	Leu Ala Ala Thr	Thr		
	620		625		630
Glu Lys Thr Glu Pro	Asn Ser Gln Glu Asp	Lys Asn Asp Gly	Gly		
	635		640		645

Lys	Ser	Arg	Lys	Gly	Asn	Ile	Glu	Leu	Ala	Ser	Ser	Glu	Pro	Gln
				650					655					660
His	Phe	Thr	Thr	Thr	Val	Thr	Arg	Cys	Ser	Pro	Thr	Val	Ala	Phe
				665					670					675
Val	Glu	Phe	Pro	Ser	Ser	Pro	Gln	Leu	Lys	Asn	Asp	Val	Ser	Glu
				680					685					690
Glu	Lys	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Glu	Met	Ser	Gly	Lys	Val
				695					700					705
Glu	Leu	Val	Leu	Ser	Gln	Lys	Val	Val	Lys	Pro	Lys	Ser	Pro	Glu
				710					715					720
Pro	Glu	Ala	Thr	Leu	Thr	Phe	Pro	Phe	Leu	Asp	Lys	Met	Pro	Glu
				725					730					735
Ala	Asn	Gln	Leu	His	Leu	Pro	Asn	Leu	Asn	Ser	Gln	Val	Asp	Ser
				740					745					750
Pro	Ser	Ser	Glu	Lys	Ser	Pro	Val	Thr	Thr	Pro	Phe	Lys	Phe	Trp
				755					760					765
Ala	Trp	Asp	Pro	Glu	Glu	Glu	Arg	Arg	Arg	Gln	Glu	Lys	Trp	Gln
				770					775					780
Gln	Glu	Gln	Glu	Arg	Leu	Leu	Gln	Glu	Arg	Tyr	Gln	Lys	Glu	Gln
				785					790					795
Asp	Lys	Leu	Lys	Glu	Glu	Trp	Glu	Lys	Ala	Gln	Lys	Glu	Val	Glu
				800					805					810
Glu	Glu	Glu	Arg	Arg	Tyr	Tyr	Glu	Glu	Glu	Arg	Lys	Ile	Ile	Glu
				815					820					825
Asp	Thr	Val	Val	Pro	Phe	Thr	Val	Ser	Ser	Ser	Ser	Ala	Asp	Gln
				830					835					840
Leu	Ser	Thr	Ser	Ser	Ser	Met	Thr	Glu	Gly	Ser	Gly	Thr	Met	Asn
				845					850					855
Lys	Ile	Asp	Leu	Gly	Asn	Cys	Gln	Asp	Glu	Lys	Gln	Asp	Arg	Arg
				860					865					870
Trp	Lys	Lys	Ser	Phe	Gln	Gly	Asp	Asp	Ser	Asp	Leu	Leu	Leu	Lys
				875					880					885
Thr	Arg	Glu	Ser	Asp	Arg	Leu	Glu	Glu	Lys	Gly	Ser	Leu	Thr	Glu
				890					895					900
Gly	Ala	Leu	Ala	His	Ser	Gly	Asn	Pro	Val	Ser	Lys	Gly	Val	His
				905					910					915
Glu	Asp	His	Gln	Leu	Asp	Thr	Glu	Ala	Gly	Ala	Pro	His	Cys	Gly
				920					925					930
Thr	Asn	Pro	Gln	Leu	Ala	Gln	Asp	Pro	Ser	Gln	Asn	Gln	Gln	Thr
				935					940					945
Ser	Asn	Pro	Thr	His	Ser	Ser	Glu	Asp	Val	Lys	Pro	Lys	Thr	Leu
				950					955					960
Pro	Leu	Asp	Lys	Ser	Ile	Asn	His	Gln	Ile	Glu	Ser	Pro	Ser	Glu
				965					970					975
Arg	Arg	Lys	Ser	Ile	Ser	Gly	Lys	Lys	Leu	Cys	Ser	Ser	Cys	Gly
				980					985					990
Leu	Pro	Leu	Gly	Lys	Gly	Ala	Ala	Met	Ile	Ile	Glu	Thr	Leu	Asn
				995					1000					1005
Leu	Tyr	Phe	His	Ile	Gln	Cys	Phe	Arg	Cys	Gly	Ile	Cys	Lys	Gly
				1010					1015					1020
Gln	Leu	Gly	Asp	Ala	Val	Ser	Gly	Thr	Asp	Val	Arg	Ile	Arg	Asn
				1025					1030					1035
Gly	Leu	Leu	Asn	Cys	Asn	Asp	Cys	Tyr	Met	Arg	Ser	Arg	Ser	Ala
				1040					1045					1050
Gly	Gln	Pro	Thr	Thr	Leu									
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<210> 31

<211> 1569

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4173970CD1

<400> 31

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Ser	Pro	Ala	Leu	Leu	Gly	Val	Gln	Lys	Ala	Val	Ser	Thr	Arg	Val
				20					25					30
Pro	Thr	Gly	Ser	Asn	Ser	Ser	Ser	Gln	Thr	Thr	Glu	Cys	Leu	Thr
				35					40					45
Pro	Glu	Ser	Cys	Ser	Gln	Thr	Thr	Ser	Asn	Val	Ala	Ser	Gln	Ser
				50					55					60
Met	Pro	Pro	Val	Tyr	Pro	Ser	Val	Asp	Ile	Asp	Ala	His	Thr	Glu
				65					70					75
Ser	Asn	His	Asp	Thr	Ala	Leu	Thr	Leu	Ala	Cys	Ala	Gly	Gly	His
				80					85					90
Glu	Glu	Leu	Val	Ser	Val	Leu	Ile	Ala	Arg	Asp	Ala	Lys	Ile	Glu
				95					100					105
His	Arg	Asp	Lys	Lys	Gly	Phe	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Thr
				110					115					120
Ala	Gly	His	Val	Gly	Val	Val	Glu	Ile	Leu	Leu	Asp	Lys	Gly	Gly
				125					130					135
Asp	Ile	Glu	Ala	Gln	Ser	Glu	Arg	Thr	Lys	Asp	Thr	Pro	Leu	Ser
				140					145					150
Leu	Ala	Cys	Ser	Gly	Gly	Arg	Gln	Glu	Val	Val	Asp	Leu	Leu	Leu
				155					160					165
Ala	Arg	Gly	Ala	Asn	Lys	Glu	His	Arg	Asn	Val	Ser	Asp	Tyr	Thr
				170					175					180
Pro	Leu	Ser	Leu	Ala	Ala	Ser	Gly	Gly	Tyr	Val	Asn	Ile	Ile	Lys
				185					190					195
Ile	Leu	Leu	Asn	Ala	Gly	Ala	Glu	Ile	Asn	Ser	Arg	Thr	Gly	Ser
				200					205					210
Lys	Leu	Gly	Ile	Ser	Pro	Leu	Met	Leu	Ala	Ala	Met	Asn	Gly	His
				215					220					225
Val	Pro	Ala	Val	Lys	Leu	Leu	Leu	Asp	Met	Gly	Ser	Asp	Ile	Asn
				230					235					240
Ala	Gln	Ile	Glu	Thr	Asn	Arg	Asn	Thr	Ala	Leu	Thr	Leu	Ala	Cys
				245					250					255
Phe	Gln	Gly	Arg	Ala	Glu	Val	Val	Ser	Leu	Leu	Asp	Arg	Arg	Lys
				260					265					270
Ala	Asn	Val	Glu	His	Arg	Ala	Lys	Thr	Gly	Leu	Thr	Pro	Leu	Met
				275					280					285
Glu	Ala	Ala	Ser	Gly	Gly	Tyr	Ala	Glu	Val	Gly	Arg	Val	Leu	Leu
				290					295					300
Asp	Lys	Gly	Ala	Asp	Val	Asn	Ala	Pro	Pro	Val	Pro	Ser	Ser	Arg
				305					310					315
Asp	Thr	Ala	Leu	Thr	Ile	Ala	Ala	Asp	Lys	Gly	His	Tyr	Lys	Phe
				320					325					330
Cys	Glu	Leu	Leu	Ile	His	Arg	Gly	Ala	His	Ile	Asp	Val	Arg	Asn
				335					340					345
Lys	Lys	Gly	Asn	Thr	Pro	Leu	Trp	Leu	Ala	Ser	Asn	Gly	Gly	His
				350					355					360
Phe	Asp	Val	Val	Gln	Leu	Leu	Val	Gln	Ala	Gly	Ala	Asp	Val	Asp
				365					370					375
Ala	Ala	Asp	Asn	Arg	Lys	Ile	Thr	Pro	Leu	Met	Ser	Ala	Phe	Arg
				380					385					390
Lys	Gly	His	Val	Lys	Val	Val	Gln	Tyr	Leu	Val	Lys	Glu	Val	Asn
				395					400					405
Gln	Phe	Pro	Ser	Asp	Ile	Glu	Cys	Met	Arg	Tyr	Ile	Ala	Thr	Ile
				410					415					420
Thr	Asp	Lys	Glu	Leu	Leu	Lys	Lys	Cys	His	Gln	Cys	Val	Glu	Thr
				425					430					435
Ile	Val	Lys	Ala	Lys	Asp	Gln	Gln	Ala	Ala	Glu	Ala	Asn	Lys	Asn
				440					445					450
Ala	Ser	Ile	Leu	Leu	Lys	Glu	Leu	Asp	Leu	Glu	Lys	Ser	Arg	Glu
				455					460					465
Glu	Ser	Arg	Lys	Gln	Ala	Leu	Ala	Ala	Lys	Arg	Glu	Lys	Arg	Lys
				470					475					480
Glu	Lys	Arg	Lys	Lys	Lys	Lys	Glu	Glu	Gln	Lys	Arg	Lys	Gln	Glu
				485					490					495
Glu	Asp	Glu	Glu	Asn	Lys	Pro	Lys	Glu	Asn	Ser	Glu	Leu	Pro	Glu

				500					505					510
Asp	Glu	Asp	Glu	Glu	Glu	Asn	Asp	Glu	Asp	Val	Glu	Gln	Glu	Val
				515					520					525
Pro	Ile	Glu	Pro	Pro	Ser	Ala	Thr	Thr	Thr	Thr	Thr	Ile	Gly	Ile
				530					535					540
Ser	Ala	Thr	Ser	Ala	Thr	Phe	Thr	Asn	Val	Phe	Gly	Lys	Lys	Arg
				545					550					555
Ala	Asn	Val	Val	Thr	Thr	Pro	Ser	Thr	Asn	Arg	Lys	Asn	Lys	Lys
				560					565					570
Asn	Lys	Thr	Lys	Glu	Thr	Pro	Pro	Thr	Ala	His	Leu	Ile	Leu	Pro
				575					580					585
Glu	Gln	His	Met	Ser	Leu	Ala	Gln	Gln	Lys	Ala	Asp	Lys	Asn	Lys
				590					595					600
Ile	Asn	Gly	Glu	Pro	Arg	Gly	Gly	Gly	Ala	Gly	Gly	Asn	Ser	Asp
				605					610					615
Ser	Asp	Asn	Leu	Asp	Ser	Thr	Asp	Cys	Asn	Ser	Glu	Ser	Ser	Ser
				620					625					630
Gly	Gly	Lys	Ser	Gln	Glu	Leu	Asn	Phe	Val	Met	Asp	Val	Asn	Ser
				635					640					645
Ser	Lys	Tyr	Pro	Ser	Leu	Leu	Leu	His	Ser	Gln	Glu	Glu	Lys	Thr
				650					655					660
Ser	Thr	Ala	Thr	Ser	Lys	Thr	Gln	Thr	Arg	Tyr	Lys	Thr	Val	Ser
				665					670					675
Leu	Pro	Leu	Ser	Ser	Pro	Asn	Ile	Lys	Leu	Asn	Leu	Thr	Ser	Pro
				680					685					690
Lys	Arg	Gly	Gln	Lys	Arg	Glu	Glu	Gly	Trp	Lys	Glu	Val	Val	Arg
				695					700					705
Arg	Ser	Lys	Lys	Leu	Ser	Val	Pro	Ala	Ser	Val	Val	Ser	Arg	Ile
				710					715					720
Met	Gly	Arg	Gly	Gly	Cys	Asn	Ile	Thr	Ala	Ile	Gln	Asp	Val	Thr
				725					730					735
Gly	Ala	His	Ile	Asp	Val	Asp	Lys	Gln	Lys	Asp	Lys	Asn	Gly	Glu
				740					745					750
Arg	Met	Ile	Thr	Ile	Arg	Gly	Gly	Thr	Glu	Ser	Thr	Arg	Tyr	Ala
				755					760					765
Val	Gln	Leu	Ile	Asn	Ala	Leu	Ile	Gln	Asp	Pro	Ala	Lys	Glu	Leu
				770					775					780
Glu	Asp	Leu	Ile	Pro	Lys	Asn	His	Ile	Arg	Thr	Pro	Ala	Ser	Thr
				785					790					795
Lys	Ser	Ile	His	Ala	Asn	Phe	Ser	Ser	Gly	Val	Gly	Thr	Thr	Ala
				800					805					810
Ala	Ser	Ser	Lys	Asn	Ala	Phe	Pro	Leu	Gly	Ala	Pro	Thr	Leu	Val
				815					820					825
Thr	Ser	Gln	Ala	Thr	Thr	Leu	Ser	Thr	Phe	Gln	Pro	Ala	Asn	Lys
				830					835					840
Leu	Asn	Lys	Asn	Val	Pro	Thr	Asn	Val	Arg	Ser	Ser	Phe	Pro	Val
				845					850					855
Ser	Leu	Pro	Leu	Ala	Tyr	Pro	His	Pro	His	Phe	Ala	Leu	Leu	Ala
				860					865					870
Ala	Gln	Thr	Met	Gln	Gln	Ile	Arg	His	Pro	Arg	Leu	Pro	Met	Ala
				875					880					885
Gln	Phe	Gly	Gly	Thr	Phe	Ser	Pro	Ser	Pro	Asn	Thr	Trp	Gly	Pro
				890					895					900
Phe	Pro	Val	Arg	Pro	Val	Asn	Pro	Gly	Asn	Thr	Asn	Ser	Ser	Pro
				905					910					915
Lys	His	Asn	Asn	Thr	Ser	Arg	Leu	Pro	Asn	Gln	Asn	Gly	Thr	Val
				920					925					930
Leu	Pro	Ser	Glu	Ser	Ala	Gly	Leu	Ala	Thr	Ala	Ser	Cys	Pro	Ile
				935					940					945
Thr	Val	Ser	Ser	Val	Val	Ala	Ala	Ser	Gln	Gln	Leu	Cys	Val	Thr
				950					955					960
Asn	Thr	Arg	Thr	Pro	Ser	Ser	Val	Arg	Lys	Gln	Leu	Phe	Ala	Cys
				965					970					975
Val	Pro	Lys	Thr	Ser	Pro	Pro	Ala	Thr	Val	Ile	Ser	Ser	Val	Thr
				980					985					990
Ser	Thr	Cys	Ser	Ser	Leu	Pro	Ser	Val	Ser	Ser	Ala	Pro	Ile	Thr
				995					1000					1005

Ser Gly Gln Ala Pro	Thr Thr Phe Leu Pro	Ala Ser Thr Ser Gln	
1010	1015	1020	
Ala Gln Leu Ser Ser	Gln Lys Met Glu Ser	Phe Ser Ala Val Pro	
1025	1030	1035	
Pro Thr Lys Glu Lys	Val Ser Thr Gln Asp	Gln Pro Met Ala Asn	
1040	1045	1050	
Leu Cys Thr Pro Ser	Ser Thr Ala Asn Ser	Cys Ser Ser Ser Ala	
1055	1060	1065	
Ser Asn Thr Pro Gly	Ala Pro Glu Thr His	Pro Ser Ser Ser Pro	
1070	1075	1080	
Thr Pro Thr Ser Ser	Asn Thr Gln Glu Glu	Ala Gln Pro Ser Ser	
1085	1090	1095	
Val Ser Asp Leu Ser	Pro Met Ser Met Pro	Phe Ala Ser Asn Ser	
1100	1105	1110	
Glu Pro Ala Pro Leu	Thr Leu Thr Ser Pro	Arg Met Val Ala Ala	
1115	1120	1125	
Asp Asn Gln Asp Thr	Ser Asn Leu Pro Gln	Leu Ala Val Pro Ala	
1130	1135	1140	
Pro Arg Val Ser His	Arg Met Gln Pro Arg	Gly Ser Phe Tyr Ser	
1145	1150	1155	
Met Val Pro Asn Ala	Thr Ile His Gln Asp	Pro Gln Ser Ile Phe	
1160	1165	1170	
Val Thr Asn Pro Val	Thr Leu Thr Pro Pro	Gln Gly Pro Pro Ala	
1175	1180	1185	
Ala Val Gln Leu Ser	Ser Ala Val Asn Ile	Met Asn Gly Ser Gln	
1190	1195	1200	
Met His Ile Asn Pro	Ala Asn Lys Ser Leu	Pro Pro Thr Phe Gly	
1205	1210	1215	
Pro Ala Thr Leu Phe	Asn His Phe Ser Ser	Leu Phe Asp Ser Ser	
1220	1225	1230	
Gln Val Pro Ala Asn	Gln Gly Trp Gly Asp	Gly Pro Leu Ser Ser	
1235	1240	1245	
Arg Val Ala Thr Asp	Ala Ser Phe Thr Val	Gln Ser Ala Phe Leu	
1250	1255	1260	
Gly Asn Ser Val Leu	Gly His Leu Glu Asn	Met His Pro Asp Asn	
1265	1270	1275	
Ser Lys Ala Pro Gly	Phe Arg Pro Pro Ser	Gln Arg Val Ser Thr	
1280	1285	1290	
Ser Pro Val Gly Leu	Pro Ser Ile Asp Pro	Ser Gly Ser Ser Pro	
1295	1300	1305	
Ser Ser Ser Ser Ala	Pro Leu Ala Ser Phe	Ser Gly Ile Pro Gly	
1310	1315	1320	
Thr Arg Val Phe Leu	Gln Gly Pro Ala Pro	Val Gly Thr Pro Ser	
1325	1330	1335	
Phe Asn Arg Gln His	Phe Ser Pro His Pro	Trp Thr Ser Ala Ser	
1340	1345	1350	
Asn Ser Cys Asp Ser	Pro Ile Pro Ser Val	Ser Ser Gly Ser Ser	
1355	1360	1365	
Ser Pro Leu Ser Ala	Thr Ser Ala Pro Pro	Thr Leu Gly Cln Pro	
1370	1375	1380	
Lys Gly Val Ser Ala	Ser Gln Asp Arg Lys	Ile Pro Pro Pro Ile	
1385	1390	1395	
Gly Thr Glu Arg Leu	Ala Arg Ile Arg Gln	Gly Gly Ser Val Ala	
1400	1405	1410	
Gln Ala Pro Ala Gly	Thr Ser Phe Val Ala	Pro Val Gly His Ser	
1415	1420	1425	
Gly Ile Trp Ser Phe	Gly Val Asn Ala Val	Ser Glu Gly Leu Ser	
1430	1435	1440	
Gly Trp Ser Gln Ser	Val Met Gly Asn His	Pro Met His Gln Gln	
1445	1450	1455	
Leu Ser Asp Pro Ser	Thr Phe Ser Gln His	Gln Pro Met Glu Arg	
1460	1465	1470	
Asp Asp Ser Gly Met	Val Ala Pro Ser Asn	Ile Phe His Gln Pro	
1475	1480	1485	
Met Ala Ser Gly Phe	Val Asp Phe Ser Lys	Gly Leu Pro Ile Ser	
1490	1495	1500	
Met Tyr Gly Gly Thr	Ile Ile Pro Ser His	Pro Gln Leu Ala Asp	

	1505		1510		1515
Val	Pro	Gly	Gly	Pro	Leu
	1520		1525		1530
Ala	Trp	Asn	Pro	Met	Ile
	1535		1540		1545
Thr	Asp	Ala	Gln	Gln	Ile
	1550		1555		1560
Gly	Asn	Met	His	Leu	Lys
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<210> 32
 <211> 680
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2772751CD1

<400> 32

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Val	Cys	Ala	Phe	Val	Thr	Asn	Gln	Arg	Thr	His	Glu	Gln	Met	Gly
			20						25					30
Pro	Ser	Ile	Glu	Ala	Met	Pro	Glu	Thr	Leu	Leu	Ser	Leu	Trp	Gly
			35						40					45
Leu	Val	Ser	Asp	Val	Pro	Gln	Glu	Leu	Gln	Ala	Val	Ala	Gln	Gln
			50						55					60
Phe	Ser	Leu	Pro	Gln	Glu	Gln	Val	Ser	Glu	Glu	Leu	Asp	Gly	Val
			65						70					75
Gly	Val	Ser	Ile	Gly	Ser	Ala	Ile	His	Thr	Gln	Leu	Arg	Ser	Ser
			80						85					90
Val	Tyr	Pro	Leu	Leu	Ala	Ala	Val	Gly	Ser	Leu	Gly	Gln	Val	Leu
			95						100					105
Gln	Val	Ser	Val	His	His	Leu	Gln	Thr	Leu	Asn	Ala	Thr	Val	Val
			110						115					120
Glu	Leu	Gln	Ala	Gly	Gln	Gln	Asp	Leu	Glu	Pro	Ala	Ile	Arg	Glu
			125						130					135
His	Arg	Asp	Arg	Leu	Leu	Glu	Leu	Leu	Gln	Glu	Ala	Arg	Cys	Gln
			140						145					150
Gly	Asp	Cys	Ala	Gly	Ala	Leu	Ser	Trp	Ala	Arg	Thr	Leu	Glu	Leu
			155						160					165
Gly	Ala	Asp	Phe	Ser	Gln	Val	Pro	Ser	Val	Asp	His	Val	Leu	His
			170						175					180
Gln	Leu	Lys	Gly	Val	Pro	Glu	Ala	Asn	Phe	Ser	Ser	Met	Val	Gln
			185						190					195
Glu	Glu	Asn	Ser	Thr	Phe	Asn	Ala	Leu	Pro	Ala	Leu	Ala	Ala	Met
			200						205					210
Gln	Thr	Ser	Ser	Val	Val	Gln	Glu	Leu	Lys	Lys	Ala	Val	Ala	Gln
			215						220					225
Gln	Pro	Glu	Gly	Val	Arg	Thr	Leu	Ala	Glu	Gly	Phe	Pro	Gly	Leu
			230						235					240
Glu	Ala	Ala	Ser	Arg	Trp	Ala	Gln	Ala	Leu	Gln	Glu	Val	Glu	Glu
			245						250					255
Ser	Ser	Arg	Pro	Tyr	Leu	Gln	Glu	Val	Gln	Arg	Tyr	Glu	Thr	Tyr
			260						265					270
Arg	Trp	Ile	Val	Gly	Cys	Val	Leu	Cys	Ser	Val	Val	Leu	Phe	Val
			275						280					285
Val	Leu	Cys	Asn	Leu	Leu	Gly	Leu	Asn	Leu	Gly	Ile	Trp	Gly	Leu
			290						295					300
Ser	Ala	Arg	Asp	Asp	Pro	Ser	His	Pro	Glu	Ala	Lys	Gly	Glu	Ala
			305						310					315
Gly	Ala	Arg	Phe	Leu	Met	Ala	Gly	Val	Gly	Leu	Ser	Phe	Leu	Phe
			320						325					330
Ala	Ala	Pro	Leu	Ile	Leu	Leu	Val	Phe	Ala	Thr	Phe	Leu	Val	Gly
			335						340					345
Gly	Asn	Val	Gln	Thr	Leu	Val	Cys	Gln	Ser	Trp	Glu	Asn	Ser	Glu

Leu Phe Glu Phe	350	Asn Leu Pro Pro Ser	355	Met	360
Asn Leu Ser Gln	365	Lys Asn Ile Ser Ile	370	His	375
Gln Ala Tyr Gln	380	Ala Ala Leu Trp Thr	385	Val	390
Leu Gln Leu Asn	395	Glu Glu His Leu Asp	400	Ile	405
Asn Gln Tyr Thr	410	Glu Leu Gln Ser Leu	415	Lys	420
Val Asp Thr Gln	425	Ser Ser Ala Ala Arg	430	Arg	435
Asp Leu Glu Ala	440	Leu Gln Arg Ile His	445	Tyr	450
Pro Asp Phe Leu	455	Pro Val Val Lys Thr	460	Ser	465
Met Glu Gln Leu	470	Gly Leu Ala Gln Ala	475	Gln	480
Asp Asn Ser Val	485	Gln Glu Glu Ala Gln	490	Gly	495
Leu Arg Asn Leu	500	Val Pro Gln Gln Ser	505	Leu	510
Val Ala Lys Leu	515	Ala Leu Glu Ser Ser	520	Ala	525
Pro Asn Leu Gln	530	Val Leu Ala Asn Val	535	Thr	540
Tyr Leu Lys Gly	545	Ala Ala Arg Ile Leu	550	Arg	555
Asn Val Ser Glu	560	Glu Met Gly Tyr Phe	565	Ser	570
Gln Tyr Val Ala	575	Val Thr Gln Arg Ile	580	Ala	585
Thr Cys Gln Pro	590	Asp Asn Ser Arg Val	595	Ile	600
Leu Cys Asp Met	605	Asn Ala Phe Trp Phe	610	Cys	615
Leu Ala Trp Cys	620	Pro Ser Ile Ile Phe	625	Ala	630
Val Lys Thr Ser	635	Ile Arg Lys Arg Leu	640	Ser	645
Ser Thr Ser Ser	650	Phe His Ile Pro Arg	655	Val	660
Thr Ser Leu Lys	665		670		675
	680				

<210> 33
 <211> 590
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2793768CD1

<400> 33
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 Leu Val Trp Lys Asn Asp Tyr Arg Gln Leu Glu Lys Glu Leu Gln
 20 25 30
 Gly Gln Asn Val Glu Ala Val Asp Pro Arg Gly Arg Thr Leu Leu
 35 40 45
 His Leu Ala Val Ser Leu Gly His Leu Glu Ser Ala Arg Val Leu
 50 55 60
 Leu Arg His Lys Ala Asp Val Thr Lys Glu Asn Arg Gln Gly Trp
 65 70 75
 Thr Val Leu His Glu Ala Val Ser Thr Gly Asp Pro Glu Met Val

				80					85					90
Tyr	Thr	Val	Leu	Gln	His	Arg	Asp	Tyr	His	Asn	Thr	Ser	Met	Ala
				95					100					105
Leu	Glu	Gly	Val	Pro	Glu	Leu	Leu	Gln	Lys	Ile	Leu	Glu	Ala	Pro
				110					115					120
Asp	Phe	Tyr	Val	Gln	Met	Lys	Trp	Glu	Phe	Thr	Ser	Trp	Val	Pro
				125					130					135
Leu	Val	Ser	Arg	Ile	Cys	Pro	Asn	Asp	Val	Cys	Arg	Ile	Trp	Lys
				140					145					150
Ser	Gly	Ala	Lys	Leu	Arg	Val	Asp	Ile	Thr	Leu	Leu	Gly	Phe	Glu
				155					160					165
Asn	Met	Ser	Trp	Ile	Arg	Gly	Arg	Arg	Ser	Phe	Ile	Phe	Lys	Gly
				170					175					180
Glu	Asp	Asn	Trp	Ala	Glu	Leu	Met	Glu	Val	Asn	His	Asp	Asp	Lys
				185					190					195
Val	Val	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ser	Gln	Glu	Met	Glu	Arg
				200					205					210
Leu	Thr	Leu	Asp	Leu	Met	Lys	Pro	Lys	Ser	Arg	Glu	Val	Glu	Arg
				215					220					225
Arg	Leu	Thr	Ser	Pro	Val	Ile	Asn	Thr	Ser	Leu	Asp	Thr	Lys	Asn
				230					235					240
Ile	Ala	Phe	Glu	Arg	Thr	Lys	Ser	Gly	Phe	Trp	Gly	Trp	Arg	Thr
				245					250					255
Asp	Lys	Ala	Glu	Val	Val	Asn	Gly	Tyr	Glu	Ala	Lys	Val	Tyr	Thr
				260					265					270
Val	Asn	Asn	Val	Asn	Val	Ile	Thr	Lys	Ile	Arg	Thr	Glu	His	Leu
				275					280					285
Thr	Glu	Glu	Glu	Lys	Lys	Arg	Tyr	Lys	Ala	Asp	Arg	Asn	Pro	Leu
				290					295					300
Glu	Ser	Leu	Leu	Gly	Thr	Val	Glu	His	Gln	Phe	Gly	Ala	Gln	Gly
				305					310					315
Asp	Leu	Thr	Thr	Glu	Cys	Ala	Thr	Ala	Asn	Asn	Pro	Thr	Ala	Ile
				320					325					330
Thr	Pro	Asp	Glu	Tyr	Phe	Asn	Glu	Glu	Phe	Asp	Leu	Lys	Asp	Arg
				335					340					345
Asp	Ile	Gly	Arg	Pro	Lys	Glu	Leu	Thr	Ile	Arg	Thr	Gln	Lys	Phe
				350					355					360
Lys	Ala	Met	Leu	Trp	Met	Cys	Glu	Glu	Phe	Pro	Leu	Ser	Leu	Val
				365					370					375
Glu	Gln	Val	Ile	Pro	Ile	Ile	Asp	Leu	Met	Ala	Arg	Thr	Ser	Ala
				380					385					390
His	Phe	Ala	Arg	Leu	Arg	Asp	Phe	Ile	Lys	Leu	Glu	Phe	Pro	Pro
				395					400					405
Gly	Phe	Pro	Val	Lys	Ile	Glu	Ile	Pro	Leu	Phe	His	Val	Leu	Asn
				410					415					420
Ala	Arg	Ile	Thr	Phe	Gly	Asn	Val	Asn	Gly	Cys	Ser	Thr	Ala	Glu
				425					430					435
Glu	Ser	Val	Ser	Gln	Asn	Val	Glu	Gly	Thr	Gln	Ala	Asp	Ser	Ala
				440					445					450
Ser	His	Ile	Thr	Asn	Phe	Glu	Val	Asp	Gln	Ser	Val	Phe	Glu	Ile
				455					460					465
Pro	Glu	Ser	Tyr	Tyr	Val	Gln	Asp	Asn	Gly	Arg	Asn	Val	His	Leu
				470					475					480
Gln	Asp	Glu	Asp	Tyr	Glu	Ile	Met	Gln	Phe	Ala	Ile	Gln	Gln	Ser
				485					490					495
Leu	Leu	Glu	Ser	Ser	Arg	Ser	Gln	Glu	Leu	Ser	Gly	Pro	Ala	Ser
				500					505					510
Asn	Gly	Gly	Ile	Ser	Gln	Thr	Asn	Thr	Tyr	Asp	Ala	Gln	Tyr	Glu
				515					520					525
Arg	Ala	Ile	Gln	Glu	Ser	Leu	Leu	Thr	Ser	Thr	Glu	Gly	Leu	Cys
				530					535					540
Pro	Ser	Ala	Leu	Ser	Glu	Thr	Ser	Arg	Phe	Asp	Asn	Asp	Leu	Gln
				545					550					555
Leu	Ala	Met	Glu	Leu	Ser	Ala	Lys	Glu	Leu	Glu	Glu	Trp	Glu	Leu
				560					565					570
Arg	Leu	Gln	Glu	Glu	Glu	Ala	Glu	Leu	Gln	Gln	Val	Leu	Gln	Leu
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Ser Leu Thr Asp Lys
590

<210> 34
<211> 315
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 3035248CD1

<400> 34
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20 25 30
Ala Asp Gly Glu Pro Leu His Asn Glu Glu Glu Arg Ala Gly Ala
35 40 45
Gly Gln Val Gly Arg Ser Leu Pro Gln Glu Ser Glu Glu Gln Arg
50 55 60
Thr Gly Ser Arg Pro Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu
65 70 75
Gln Ala Gln Arg Arg Ala Gln Arg Val Ala Trp Glu Asp Gly Asp
80 85 90
Glu Asn Val Gly Gln Thr Val Ile Pro Ala Gln Glu Glu Glu Gly
95 100 105
Ile Glu Lys Pro Ala Glu Val His Pro Thr Gly Lys Ile Gly Ala
110 115 120
Lys Lys Leu Arg Lys Leu Glu Glu Lys Gln Ala Arg Lys Ala Gln
125 130 135
Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu Arg Lys Arg Leu Glu
140 145 150
Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu Glu Arg Leu Arg
155 160 165
Leu Lys Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys Ala Gln Glu
170 175 180
Glu Gln Ala Arg Arg Asp His Glu Glu Tyr Leu Lys Leu Lys Glu
185 190 195
Ala Phe Val Val Glu Glu Gly Val Ser Glu Thr Met Thr Glu
200 205 210
Glu Gln Ser His Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
215 220 225
Lys Ser Lys Val Val Leu Leu Glu Asp Leu Ala Phe Gln Met Gly
230 235 240
Leu Arg Thr Gln Asp Ala Ile Asn Arg Ile Gln Asp Leu Leu Thr
245 250 255
Glu Gly Thr Leu Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile
260 265 270
Tyr Ile Thr Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg
275 280 285
Gln Arg Gly Arg Val Ser Ile Thr Glu Leu Ala Gln Ala Ser Asn
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Ser Leu Ile Ser Trp Gly Gln Asp Leu Pro Ala Gln Ala Ser Ala
305 310 315

<210> 35
<211> 2345
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 1889577CB1

<400> 35

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gagatcgtgc tgggcaccaa ggctgtcatc cagggactgg agactctgcg tggggagcat 180
cgtgccctgc tggctcctct gggtgcacct gaggcggcg aacccgagcc tggctcgag 240
gagcgcgtga tctcctgcg tcgctccctg gagccattg agcttgggct gggggaggcc 300
caggtgatct tggcattgtc gagccacctg ggggctgtag aatcagagaa gcagaagctg 360
cgggcgcagg tggcgctctt ggtgcaggag aaccagtggc tgcgtgagga gctggcgggg 420
acacagcaga agctgcagcg cagtgcagag gccgtggccc agctcgagga ggagaagcag 480
cacttgctgt tcatgagcca gatccgcaag ttggatgaag acgcctcccc taacgaggag 540
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gttat
2345

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<210> 36
 <211> 709
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2427982CB1

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<400> 36
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attcccccta tagagaagat ggatgcatcc ttgtccatgc ttgctaattg cgagaagctt 180
tactgtctca caaactgcat tgaaaaaatt gccaacctga atggcttaaa aaacttgagg 240
atattatctt taggaagaaa caacataaag aacttaaatg gactggaggc agtaggggac 300
acattagaag aactgtggat ctctacaat tttattgaga agttgaaagg gatccacata 360
atgaagaaat tgaagattct ctacatgtct aataacctgg taaaagactg ggctgagttt 420
gtgaagctgg cagaactgcc atgcctcgaa gacctggtgt ttgtaggcaa tcccttgga 480
gagaaacatt tgcctgagaa taactggatt gaagaagcaa ccaagagagt gcccaactg 540
aaaaagctgg atggtactcc agtaattaaa ggggatgagg aagaagacaa ctaatgccac 600
gctttccact gtgtgttaac ttattttaa gtcataagaa caatagataa attttatata 660
attgtctatt ttaaagattc tgtatgggac aaaagtttct taagataaa 709

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<210> 37
 <211> 1569
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2470833CB1

<400> 37

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agcttcactt tcacggcatc cccccccctc gggccctgcc gcagagagga ggaagctcct 180
gccggctgag cgggcctgga ggaagtgagc agcggggctc ctgcctcccg gcctggtccc 240
cgaagacccc agaagaacct ggaacttgct tccattcgga atccaggac caccctttgc 300
actcagtagg cttttgtttt cctgcgtgga aagcgggttg gcttgggagg cgatggagcc 360
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gctctcaaaa ggaggaaaga agaaatacct gccaccact tcccgaagg accccaaatt 480
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tgtgtccgc agcctggagg aggacatgtt cgacgggctc atcctacacc acctattcca 600
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gcacaagctc acagtgtgtc tggaggccgt gaaccggagt ctgcagctgg aggagtggca 720
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tgaacccctt tgtgtggatc attttgagcc gcctggcctt gctcagttta ttttaataaa 1560
agtatttct 1569
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<210> 38

<211> 1172

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2080579CB1

<400> 38

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ggcggcgtgg tgggtgacca ggacgactac tgctccggct cggtgatgtc ggagcgggtg 180
tcgggcctgg cgggctccat ctaccgcgag ttcgagcgcc tcattccactg ctacgacgag 240
gaggtggtca aggagctcat gccgctggtg gtgaacgtgc tggagaacct agactcgggtg 300
ctcagcgaga accaggagca cgaggtggag ctggagctgc tgcgcgagga caacgagcag 360
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gagtttgaag atgctctgga acaagagaag aaagagctgc aaatccaggt ggagcactac 480
gagttccaga cgcgccagct ggagctgaag gccaaagaat atgccgatca gatttccggg 540
ttggaggagc gggagtccga gatgaagaag gagtacaatg ccctgcacca gcggcacaca 600
gagatgatac agacctacgt ggagcacatt gagaggcca agatgcagca ggtcggagga 660
aacagccaga ccgagagcag cctgccgggg cgagggtacg cggggcgcg cggggtggag 720
gtacgcgggg cgcggcgggg cggaggtag caggacgcgg cacatgccag ggtcgtagt 780
cttggttatg cccgcgctct gggtcagga tgacagggaa cactctggag acccaggagg 840
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cagcttgccg atatttaacc cttactatcc acagattctg tgtttgcaaa tgtatctact 1020
cgctaaaata tatctgtgac ctacgcgggg cacagtgaat tatgcctgta atcctagaac 1080
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ccagcaagat cttgtctcta caaaaaaaaa aa 1172
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<210> 39

<211> 2380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2156553CB1

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<210> 49

<211> 2163

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1315267CB1

<400> 49

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<210> 50

<211> 1615

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1403289CB1

<400> 50

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<210> 51

<211> 1356

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1607607CB1

<400> 51

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<210> 52

<211> 1268

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1660025CB1

<400> 52

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<210> 53

<211> 2554

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1796836CB1

<400> 53

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<210> 54

<211> 1216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2880670CB1

<400> 54

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1216

<210> 55

<211> 1457

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 2913976CB1

<400> 55

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<210> 56

<211> 1636

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3092084CB1

<400> 56

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<210> 57

<211> 1742

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 3882482CB1

<400> 57

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<210> 58

<211> 602

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4933451CB1

<400> 58

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<210> 59

<211> 3237

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5043904CB1

<400> 59

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<211> 3640

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5202390CB1

<400> 60

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<211> 2111

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5526375CB1

<400> 61

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(74) Agents: **HAMLET-COX, Diana** et al.; Incyte Genomics, Inc., 3160 Porter Drive, Palo Alto, CA 94304 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW). Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM). European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR). OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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- with international search report
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(54) Title: CYTOSKELETON-ASSOCIATED PROTEINS

(57) Abstract: The invention provides human cytoskeleton-associated proteins (CYSKP) and polynucleotides which identify and encode CYSKP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of CYSKP.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/14355

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/10 C12Q1/68 C07K14/47 C07K14/705
C07K16/18 C07K16/28 A01K67/027 A61K38/17 A61K39/395
G01N33/53 G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q C07K A01K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 45436 A (GENETICS INST) 15 October 1998 (1998-10-15)	1,3,6-44
Y	see seq.ID.1493.	2,4,5
X	RAHMAN AMENA ET AL: "Two kinesin light chain genes in mice. Identification and characterization of the encoded proteins." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 25, 19 June 1998 (1998-06-19), pages 15395-15403, XP002187123 ISSN: 0021-9258	1,3,6-44
Y	the whole document	2,4,5
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

11 January 2002

Date of mailing of the international search report

25 04 2002

Name and mailing address of the ISA

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Authorized officer

Smalt, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/14355

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] Entry/Acc.no. AW249420, 7 January 2000 (2000-01-07) STRAUSBERG, R.: "2819569.5prime NIH_MGC_7 Homo sapiens cDNA clone 2819569 5', mRNA sequence." XP002187124 the whole document	1,3,6-44
A	--- MANN S S ET AL: "MOLECULAR CHARACTERIZATION OF LIGHT CHAIN 3" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 269, no. 15, 15 April 1994 (1994-04-15), pages 11492-11497, XP002067017 ISSN: 0021-9258 cited in the application the whole document	
A	--- SPILLANTINI M G ET AL: "TAU PROTEIN PATHOLOGY IN NEURODEGENERATIVE DISEASES" TRENDS IN NEUROSCIENCE, ELSEVIER, AMSTERDAM, NL, vol. 21, no. 10, 1998, pages 428-433, XP000946483 ISSN: 0166-2236 cited in the application the whole document	
A	--- MOORE J D ET AL: "KINESIN PROTEINS: A PHYLUM OF MOTORS FOR MICROTUBULE-BASED MOTILITY" BIOESSAYS, CAMBRIDGE, GB, vol. 18, no. 3, 1996, pages 207-219, XP000952735 ISSN: 0265-9247 cited in the application the whole document	
P,X	--- WO 01 12659 A (GERMAN HUMAN GENOME PROJECT ;WIEMANN STEFAN (DE)) 22 February 2001 (2001-02-22) see seq.ID's 814 and 815.	1,3, 6-16,30, 31,35-44
P,X	--- EP 1 074 617 A (HELIX RES INST) 7 February 2001 (2001-02-07) see seq.ID's 14839, 14840, 17059, 17060.	1,3, 6-16,30, 31,35-44
P,X	--- WO 00 65340 A (MYRIAD GENETICS INC) 2 November 2000 (2000-11-02) see seq.ID.7 -----	1,3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/14355

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 18 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 20,21,23,24
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-44 (partially); 45, 79 (complete)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 20,21,23,24

Present claims 20,21,23,24 relate to products defined by reference to a desirable characteristic or property, namely having (ant)agonistic activity towards the protein(s) of claim 1.

The application provides no support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for any such products. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the product/compound/method/apparatus by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search impossible. Consequently, the present search report does not extend to said claims.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: claims 45 and 79 completely,
and 1-44 partially

Polypeptide according to seq.ID.1 and variants thereof, nucleic acid encoding it or fragments comprising at least 60 contiguous nucleotides thereof, expression vector comprising said nucleic acid, host or transgenic comprising said nucleic acid, method for production of the protein, antibody directed to said polypeptide, methods for detecting the polypeptide and/or the nucleic acid, methods for identifying (ant)agonists and/or binding agents and/or activity modulators of said polypeptide or expression modulators of said nucleic acid, method for assessing toxicity, method of diagnosing a disease associated with altered expression of said polypeptide/nucleic acid using said antibody or said nucleic acid, compositions of the polypeptide or the antibody.

2. Claims: Inventions 2-34: claims 1-44 partially,
and claims 46-78 and 80-112 as far as applicable

Subject matter as defined for invention 1, but limited to the respective polypeptide sequences 2-34, whereby the seq.ID number corresponds to the number of the invention.

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/14355

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